

248 GACCTCTTACTTAAAGCTCTAGAACCCACTACGGATCTCACTGTTGTT 307
 79 LeuSerPheGlyAlaGlyAspLysThrTrpAspAlaLeuPheGluGlnAla 98
 :
 Db TCGACTTCGGCCAGGAGATGGAAACCGATGATACTCAGGCTTCAGAAGCA 367
 Qy 99 TrpAlaGluAlaCysSerSerArgThrProValGlnPheValValProLysAla 118
 :
 Db 368 TGGAGGAAGGCATGTGTCACAAATGGAGTTACTACTTCCTAAAGGAAGACT 5
 Qy 119 TyrIleLeuLeuIleGlnIleThrPheSerGlyProCysArgSerSerValIle 138
 :
 Db 428 TAICCTCTTAACTCTTAACTAGATTGAGTCAGGCCATGCAACTTTCAGTGCTCAGATC 487
 Qy 158 IleAlaPheAlpSerValGlnAsnLeuValValGlyGlyGly----GlyThrIleAsn 175
 :
 Db 548 CTATTGAGAGCTTAATCTCATGAGGGCTCGGGAGATGAGTGTG 607
 Qy 176 GlyIleGlyGlnValValTrpTrpProSerSerCysLysIleAsnLeuSerIleAsn 195
 :
 Db 608 GGCAGCAAGGAAATACTTGGTCAAACTCATGAGTCAGGCCATGCAACTTACAGCAGATC 667
 Qy 196 AspAlaProThrAlaLeuThrPheTrpAspCysLysAsnLeuLeuLeuValAsnAsnLeuLys 215
 :
 Db 668 AAAGGCCAACGGCTTACTCTCTCACACCTAAAGATTGAGATGGAAACTCTGAGA 727
 Qy 216 SerIleAsnAlaGlnGlnIleHistIleLeuPheGluSerCysThrAsnValValAlaSer 235
 :
 Db 728 GTGAGGAAATCACAACAGATTCAGTTCTGAGAAATGCCAACATGTCAGCCACAGCTTACAGCAGATC 787
 Qy 236 AspIleMetIleAsnAlaSerAlaSerAlaSerProAsnThrAspGlyValHisValSerAsn 255
 :
 Db 788 AATGTTAAGTCACTCTCTGGCCATAGTCCCACAGCTTACAGTGTATATCTGGCTTAAG 847
 Qy 256 ThrGlnItyrLeGinIleSerAspThrIleLeuGlyThrdIyAspPheCysIleSerIle 275
 :
 Db 848 ACTAAAAACATTCGATCTCAATTCAGATTCAGATTGGAGACAGTGATGTTATCCATT 907
 Qy 276 ValSerGlySerGlnAsnValGlnAlaThrAsnIleThrCysGlyProGlyHisGlyIle 295
 :
 Db 908 GAGGTGGATTCGCAAAATGTCAAATCAATGATTAATCTGACTTCGGCCCGCTCATGGATC 967
 Qy 296 SerIleGlySerLeuGlySerGlySerGluAlaTyroValSerAsnValThrValAsn 315
 :
 Db 968 AGCATTTGGAGCTTGGGGTAGACCATTCAAAGCTTATGCCGAAATGTATGGAT 1027
 Qy 316 GluIalAspIleIleGlyIlaIleGluGlyValArgIleLysThrTrpGlnGlySer 335
 :
 Db 1028 GGTCTTACGCTCTCTGAGATGACATGGAGTAACTACGGGGCTCA 1087
 Qy 336 GlyGlnAlaSerAsnIleLysPheLeuAsnValGluMetGlnAspValIleLysProle 355
 :
 Db 1088 GGAACTGCTTAACTTCAAACATCTCTATGGATAATGTCAGATCGATC 1147
 Qy 356 IleLeuAspGlnIleAspIleGlySerGlySerGluAlaSerGlySerAsp 375
 :
 Db 1148 ATATTCGACCAAGATCTACGGACAG---GACAATGGCAACGCGAGATCTGGTT 1204
 Qy 376 GlyValValAlaValValValGluAlaIleGlyIleSerIleLeuValAlaIle 395
 :
 Db 1205 CAAGGAACTATGGTGTATGAGCATTAAGGTTACGGGCTACAGTGTGGATA 1264
 Qy 396 LysPheIleAspCysSerThrAsnPheProCysIleGlyIleIleMetGluIleAsnLeu 415
 :
 Db 1265 ATGTTAATGTCAGCTGTAATATCATGCCAAAGGTATGCTGCTCTGCTGCAAGCTTGAGTGCAGTA 228
 Qy 416 ValGlyGlySerGlyLysProSerGluAlaThrCysIleAsnValHisPheAsnAla 435
 :
 Db 1325 AAAGCA-----GGAAAGCTCTTCGGAAATGTCATGTTAGCAATAA 1269

pred.	No.:	7.15e-83	Length:	1726
Score:		787.00	Matches:	168
Percent Similarity:		58.04%	Misclassifications:	73
Best Local Similarity:		40.48%	Mismatches:	160
Query Match:		32.93%	Index:	14

DB: 3 Gaps: 7

US-10-691-374-2 (1-457) x US-08-467-023-133 (1-1726)

Qy 45 AahHiaappheGlnAlaTyrLeu-----SerrYrleuserlysAanileGluSer 61
 Db 105 GCAGAAAGATCAATCTGCCAAATPATGTTGACAGTGTGTCGAAMATCTAGATCG 164

Qy 62 AsnGlnAlaIleAspLysValAsp-----LysaGlyIleLysValleAsnVal 78
 Db 165 AACGGAGTTTAAGAAAGTGAGCATCTCGTCATGATGCTATCACATCTCAATGT 224

Qy 79 LeUserpheGlyAlaLysGlyArgGlyThrYrleAspAanileAlaPheGluGlnAla 98
 Db 225 GAAAGACTGCGCAGTAGGGGTTGAGACATGATGCCACAGGCAATTCAACACCA 284

Qy 99 TRPArgGlnAlaCysSerSerArgThrProValGlnPheValValProLysValLeuAsn 118
 Db 285 TGCAGAGCTGCGATGCCAAACCCATCA---GCAATGTTGCTCTGGCCAKGCGACAAA 341

Qy 119 TyrIleLeuLysGlnIleThrPreserGlyProCysArgSerSerIleSerValValLe 138
 Db 342 TTGTTGTTAACACATCTCTTCATGGCCATGCACTCTACTTCTTAAGTA 401

Qy 139 PheGlySerLeuGluAlaSerSerLysIleSerAspTyrylSASPAGLysGluLeutroIle 158
 Db 402 GATGGGATTAATGCTGCTTACCAAATCCAGCAGCTGAGATANTAGATATGTTG 461

Qy 159 AlaPheAspSerValGlnLysLeuValValGlyGlyGlyGlyIleAsnGlyAsnGly 178
 Db 462 CAGTTGCTAACTTACAGGTTTACTCTTATGGTAAGGCTAATGTTGAGCT 521

Qy 179 GlvAlvTrpTrpProSerSerCysLys---IleAsnLysSerIleAsnProCys---Arg 195
 Db 522 AAAACAATGGGGCTGCCATGTTAATGGCTGATGGCTGATGGACGAAATTGCAACAGT 581

Qy 196 ABPAlaPOTHAlaLeuThrPheTrpAlnCysAlaLeuLysValAsnLeuLys 215
 Db 582 GATAGACCAACGCCATTAATGTTTCACGGCTGATAATCAAGACCTGAA 641

Qy 216 SerIleAsnAlaLysGlnIleHisIleLysPheGluUserCysThrAsnValValIleAsn 235
 Db 642 CTATGAGACGCCAGCTTTCATTTGTTGAGGTTGCTGAGGTTGAAATCATC 701

Qy 236 AsnLeuMetIleAsnAlaSerAlaLyserProAsnThrAspGlyValIleValAsn 255
 Db 702 GGCATTAATGTTAGGCCACGCCAGACAGTCTAACACTGTGATGATGATCTTGCA 761

Qy 256 ThrGlnTyrlleGlnIleSerAspPheThrIleIleGlyThrGlyAspPheCysIleSerIle 275
 Db 762 TCTAAAACTTTCACTTACAAAGAACGCGATGAGACGGGATGACTGCTGCGATA 821

Qy 276 ValSerGlySerGlnAsnValGlnAlaThrAsnIleThrCysGlyIleProGlyHisGlyIle 295
 Db 822 GGACACGGGTCTCTAAATATGTCATGGATCTGATTCGGCTCCAGGCGATGGATA 881

Qy 295 SerIleGlySerIleGlyLysGlyAsnSerGluAlaTyrvAlvaSerAlaValThrValAsn 315
 Db 882 AGTATAGGAAAGCTGGAGGGAAACTCTAGAGCAGAGGTTCAATGTCAGCTAAAT 941

Qy 316 GluAlaIleSerIleGlyValAlaLysValArgIleLysThrPheGlyGlySer 335
 Db 942 GGGCTAAATCTAGACACAAATGCTGAGATGAACTGCAACATGCAAGGGTGGTCA 1001

Qy 336 GlyGlnAlaSerAlaIleLysPheLeuAsnValGluMetGluAspValIleTyrProIle 355
 Db 1002 GGCATGGCAGGCAATAATTGAGATGTTGAAATGATAATTGGAGAAACCCATA 1061

Db 1122 CAATCCAGAGTGACATAGAGAACTAGTGCAACAGGAGCAATT 1181

Qy 396 LysPheAspCysSerThrAsnPheProCysGluGlyIleLeuMetGluAsnIleAlaLeu 415
 Db 1182 CAACTTAACTGCTGAGCAGTGCCGCAAGATTAAGCTAAAGGATTTTG 1241Qy 416 ValGlyGluSerGlyLysProSerGluAlaThrCysBysAsnValHsPheAsnAsn--- 434
 Db 1142 AAGCTTACCTCAGGAAAT-----ATGCTCTGCTTAATGATAATGCAATGGAT 1295Qy 435 ---AlaGluHsValThrProHisCysThrSerLeuGluIleSer 448
 Db 1296 TTCACTGAGACTGCTCATCCCTGCATGCGAAGATTAGTCCAGT 1340

RESULT 7

US-08-467-023-141

; Sequence 141, Application US/08467023

; Patent No. 6030386

; GENERAL INFORMATION:

; APPLICANT: Griffeth, Irwin J.;

; APPLICANT: Pollock, Joanne;

; APPLICANT: Bond, Julian F.;

; APPLICANT: Garman, Richard D.;

; APPLICANT: Kuo, Mei-Chang;

; APPLICANT: Yeung, Siu-mei H.;

; APPLICANT: Brauer, Andrew;

; APPLICANT: Ekey, Mark A.;

; APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From

TITLE OF INVENTION: Japanese Cedar Pollen

NUMBER OF SEQUENCES: 261

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.

STREET: 610 Lincoln St

CITY: Wellesley

STATE: MA

ZIP: 02454

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #11.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,023

FILING DATE: June 6, 1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350,225

FILING DATE: December 6, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jane E. Remillard

REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 141:

SEQUENCE CHARACTERISTICS:

LENGTH: 1479 base Pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-467-023-141

Alignment Scores:

Pred. No.: 6.33e-83

Score: 786.50

Length: 1479

Matches: 165

Percent Similarity: 58.66%

Conservativeness: 72

MisMatches: 156

Indels: 11

DB: 3 Gaps: 6

US-10-691-374-2 (1-457) x US-08-467-023-141 (1-1479)

QY 53 SerTyrIleSerLysIleGluSerAsnAsnAsnAspLysValAsp----- 69
Db 31 AGTGTCTCGAAAATATTCTAGATGAACTGGAGTTAGAAAAGTGAGCATCTCGT 69
QY 70 LysAsnGlyIleLysValLeuAsnValLeuSerProGlyValAsnGlyIleLys 90
Db 91 CATGATGCCATCACACCTCTAACATGTCGAAGAATGCGCACTAGCGATGAGCA 150
QY 90 TyrAspAsnIleAlaPheGlnIalAspAsnLysAsnTyrLeuLeuLysGlnIleThrProVal 109
Db 151 GATGCCACTGGCATTACAGCTGCAGTCAGCTGCAAACCCATCA--GCA 207
QY 110 GlnPheValValProLysAsnLysAsnTyrLeuLeuLysGlnIleThrProVal 109
Db 208 ATGTRGCTTGCCAGGCGCAAGAAATTGTTGTAACATCTGCTCTCAATGCCA 267
QY 130 CysArgSerSerIleSerValLeuIlePheGlySerIleGluIleAsnSerIleSer 149
Db 268 TGCAACCCACTTACTTTAGGTAGTAGGGATAATGCTGCTACAAATCAGCG 327
QY 150 AspIleIleAspArgArgLeuPheAspSerValGlnAsnIleValValGly 169
Db 328 AGCTGGAGAAATTGCAAGATGTTGCTTGCTTGCTGCTACAGTTTACAGTAATG 387
QY 170 GlyGlyGlyThrIleAsnGlyAsnGlyGlyValTrpTrpProSerSerGlySly--Ile 188
Db 388 GPPAAAGCTGTTATGTCAGGAAAGAAACATGGCTGGCCAATGAAATGGTC 447
QY 189 AsnLySerLeuProCys----ArgAspAlaProThralAlaLeuIlePheTrpAsnCys 206
Db 448 AATGGAGGAAATTGCAAGATGCTGAGAGCTTCAATTGCTTTC 507
QY 207 LysAsnIleIleValAsnIleIuSsLysAsnAlaGlnIleHisIleAspHe 226
Db 508 ACGGGCTGATAATCCAAAGCTGAACTATGACAGCCCATTCTATTGTT 567
QY 227 GluSerCysThrAsnValValAsnIleSerAsnIleMetIleAsnAlaSerAlaIle 246
Db 568 CGGAAATTGTTAGGGAGTAAATCATGCCATTGATATACGCCACCAAGAACCT 627
QY 247 AsnThrAspCysIvalHisIvalSerAsnThrGlnIleArgIleAsnSerPro 246
Db 628 AACATGATGCAATTGATATCTCTTGCACTAAACCTCTACTAAAGAACAGCA 687
QY 267 GlyThrGlyAspPcysIleSerIleValSerGlySerGlnAsnValGlnIleAsn 286
Db 688 GAAACAGGAGGATGACTGGCTCGCTATTGGCAGGGCTCTTAATATGCTGAGGAT 747
QY 287 IleThrCysGlyProGlyHisGlyIleSerIleGlySerIleGlySerGlyAsnSerGly 306
Db 748 CTGATTCGGGTCAGGCCATGGATAGTGGCTGCTGGAGGAAACTCTGA 807
QY 307 AlaTyrValSerAsnValThrValAsnGluIalAsnIleIleGlyIalGluAsnGlyVal 326
Db 808 GCGAGGCTTCTACGGTCACTAAATGGCTAAATTCTAGACACAAATGGATA 867
QY 327 ArgIleLysIleTrpGlnGlyGlySerGlySerIleGlySerGlyAsnVal 346
Db 868 AGATCAGAAATGGAGGGTGGCTGCGCTATAATTATGAGAATT 927
QY 347 GluMetGlnIleAspValLeuAspGlnIleAsnTyrCysAspArgValGlu 366
Db 928 GAAATGATGAAATTCGGAGAACCCATATTATTAATCTGACTGACTCAGCTCT 987
QY 367 ProCysIleGlyGlnIpheSerIleValGlnIleAsnValValTyrGluAsnIleLys 386
Db 988 GCTTGCCAAACACAGGTTGCGCTTCATACTCAAGTGTGCAAGAACATAGT 1047
QY 387 GlyThrSerIleThrIleValAlaIleLysPhasPheAspCysSerThrAsnPhoProCysGlu 406

RESULT 8

US-08-467-023-140

; Sequence 140 Application US/08467023
; Patent No. 6030386

GENERAL INFORMATION:

; APPLICANT: Griffeth, Irwin J.;
; ;
; APPLICANT: Pollock, Joanne;
; ;
; APPLICANT: Bond, Julian F.;
; ;
; APPLICANT: Garmi, Richard D.;
; ;
; APPLICANT: Kuo, Mei-Chang;
; ;
; APPLICANT: Yeung, Siu-mei H.;
; ;
; APPLICANT: Brauer, Andrew;
; ;
; APPLICANT: Eke, Mark A.;
; ;
; APPLICANT: Powers, Steven P.
; ;
; TITLE OF INVENTION: Allerenic Proteins And Peptides From
; ; NUMBER OF INVENTION: Japanese Cedar Pollen
; ; NUMBER OF SEQUENCES: 261
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
; ; STREET: 610 Lincoln St
; ; CITY: Waltham
; ; STATE: MA
; ; COUNTRY: USA
; ; ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEO ID NO.: 140:

SEQUENCE CHARACTERISTICS:

LENGTH: 199 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-08-467-023-140

Alignment Scores:
Pred. No.: 9.02e-81
Score: 768.00
Percent Similarity: 59.01%
Best Local Similarity: 41.51%
Query Match: 32.13%

Length: 1395
Matches: 159
Conservative: 67
Mismatches: 149
Indels: 8

DB: 3 Gaps: 5

US-10-691-374-2 (1-457) x US-08-467-023-140 (1-1395)

Qy 71 AspGlyLileysValleAsnValleSerUserPheGlyAlaGlyAspGlyPheSerTyr 90
 10 GAGCTATCACATCTCAATGTTGAAAGTAGCGCAGTAGGGATGAAAGCATGT 69

Qy 91 AspAsnLealapheGluGlnAlaTrpAlaGluAlaCysSerSerArgThrProAln 110
 70 TGCCTGAGGCAATTCAACAGCATGCCAGCGATGCCAAACCCATCA---GCAATG 126

Qy 111 PheAlaValProlyAspNlysAsnTyrlleuLeuLysGlnIlethrPheSerGlyProCys 130
 127 TGCCTGTCAGCCAGCGAAGAACTTGAACTCTGTCATGGCCATGT 186

Db 131 ArgSerSerIleValSerValleAspIlePheAlaPheAspSerValGlnAsn 150
 187 CAACCTCACTTACTTTRAGGATGATGGATAATAGCTGCTGACAAATCCAGCAGC 246

Qy 151 TyrLysBspArgLysAlaPheAspSerValGlnAsnLeuValValGlyGly 170
 247 TGGAGGATATAAGAATGGTGAGGTGCTAACCTAACGGTTTACTCTAATGGT 306

Qy 171 GlyGlyThrIleAsnGlyAsnGlyGlnValLeuTrpProSerSerCysLys ---IleAsn 189
 307 AAAGGGTGTATTGATGGCAAGGAAACATGGGGCTGCCAATGTAATGGTCAT 366

Qy 190 LysSerLysProCys-----AspAspAlaProThrAlaLeuIleThrPheTrpAlaCys 207
 367 GGACGAGAAATTGCAACGATCGTGATGAGACCACAGCCTAAATTC3ATTTCCACG 426

Qy 208 AsnLeuLysValAsnAsnLeuLysSerIleAsnAlaGlnGlnIleHsIleLysPheGlu 227
 427 GGCTGTGATAATCCTAACGGCTGAAGACTAACTGACAGTCGCCAATTCTAGTTTGG 486

Qy 228 SerCysteAsnValValAlaSerAsnLeuMetIleAlaSerAlaLysSerProAsn 247
 487 ATTTGTGAGGAGCTAAATCATGGCATTTAGTTACGGCACCGAGAGACGTCAC 546

Db 248 ThreAspGlyValIleValSerAsnThrCinTyrIleGlnIleSerAspThrIleGly 267
 547 ACTGATGGGATTTGATATCTTGATCTAAAATCACTAACAGAGCATGAGTAGGA 606

Qy 268 ThreCysLysAspCysIleSerIleValSerGlySerGlnAsnValGlnIleThrAsnIle 287
 607 ACAGGGGTGACTCGCGTGTAGGCAACGCTCTTAATATTGATGATGGGCTG 666

Db 288 ThreCysLysProGlyHisGlyIleSerIleGlySerGlyAsnSerGluLala 307
 667 ATTGGCGTCAGGCCATGGATAGTAACTGGAGCTCTGGGGGAAACCTAGCA 726

Qy 308 TyrValSerAsnValThrValAlaGluLalaIleIleGlyIleAlaGluAspGlyValArg 327
 727 GAGGTTCATCGGTCAGCTTAATCATGACACACACAATGGATTAGA 786

Db 328 IleLysThrPheGlyGlySerGlyGlnAlaSerAsnLysPhaLeuSerValGlu 347
 787 ATCGAAACATGSCAGGGCTGGCTAGGCATGGCAAGCCATATAATTATGAGATGTGAA 846

Qy 348 MetGlnAspVallyBytProIleIleAspGlnAsnTyrcyabargArgValGluPro 367
 847 ATGATAAATTCGGAGAACCCATATAATCAATCTACGACTTCCTCGCT 906

Db 369 CysIleGlnGlnIleSerAlaValGlnValleAsnValleValtyrgluAsnIleGly 387
 907 TGCCAAAACGAGGCTCTGGGTCACATCAGATGTCACATGACAGCAATACGG 966

Qy 388 ThreSerAlaIleThrIleValAlaIleLysPheAspCysSerThrAsnProProCysGly 407
 967 ACATCAGCAACAGCAGCAACTTAATGTCAGTCAGCTGAGTGCCTGCAAGAT 1026

Qy 408 IleIleMetGlutLeuIleAsnLeuValGlyGluSerGlyIlyProSerGluValIleCys 427

RESULT 9

US-08-467-023-139

; Sequence 139 Application US/08467023

; Patent No. 600386

; GENERAL INFORMATION:

; ; APPLICANT: Griffeth, Irwin J.;

; ; APPLICANT: Pollock, Joanne;

; ; APPLICANT: Bond, Julian F.;

; ; APPLICANT: Garmi, Richard D.;

; ; APPLICANT: Kuo, Mei-Chang;

; ; APPLICANT: Yeung, Siu-mei H.;

; ; APPLICANT: Brauer, Andrew;

; ; APPLICANT: Ekdby, Mark A.;

; ; APPLICANT: Powers, Steven P.

; TITLE OF INVENTION: Allergenic Proteins And Peptides From

; NUMBER OF INVENTION: Japanese Cedar Pollen

; NUMBER OF SEQUENCES: 261

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immologic Pharmaceutical Corporation, Inc.

; STREET: 610 Lincoln St

; CITY: Waltham

; STATE: MA

; COUNTRY: USA

; ZIP: 02454

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; ; APPLICATION NUMBER: US/08/467,023

; ; FILING DATE: June 6, 1995

; ; CLASSIFICATION: 424

; ; PRIOR APPLICATION DATA:

; ; APPLICATION NUMBER: 08/350,225

; ; FILING DATE: December 6, 1994

; ; ATTORNEY/AGENT INFORMATION:

; NAME: Jane E. Remillard

; REGISTRATION NUMBER: 38,872

; REFERENCE/DOCKET NUMBER: 205.6 USDD2 (IMI-028CPD2)

; TELECOMMUNICATION INFORMATION:

; ; TELEPHONE: (617) 227-5400

; ; TELEFAX: (617) 227-5941

; ; INFORMATION FOR SEQ ID NO: 139:

; ; SEQUENCE CHARACTERISTICS:

; ; LENGTH: 1410 base pairs

; ; TYPE: nucleic acid

; ; STRANDEDNESS: single

; ; TOPOLOGY: linear

; ; MOLECULE TYPE: cDNA

US-08-467-023-139

Alignment Scores: 9,18e-01 Length: 1410

Pred. No.: 768.00 Matches: 159

Score: 59.01% Conservative: 67%

Percent Similarity: 41.51% Mismatches: 149

Best Local Similarity: 32.13% Indexes: 8

Qry 3 Gaps: 5

DB: 1027 ATAAACCTAAGTGATAATCTTGAACTTACCTCGGGAAA-----ATTCGCTTCGC 1080

Qy 428 LysAsnValHisPheAsnAsn-----AlaGluHsValThrProHsCysThrSerLeu 445

Db 1081 CTTCATGATTAATGCCAATGGTATTCTGAGCTGACCTGCATCCCTGATGAGATTAA 1140

Qy 446 GluIleSer 448

Db 1141 AGTCCAAGT 1149

71 AspGlyIleLysValIleAsnLeuSerPheGlyAlaLysGlyAspGlyLysThrTyr 90
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 25 GATGTATACACATCTCACTGAAAGTATGGCGCAGTAGGAACTGAT 84
 91 AsparagineAlaPheGluGlnAlaTrpAsnGluAlaCysSerSerArgThrProValIn 110
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 85 TGCACGTGAGCATTTCAACAGATGGCAGCTGATGCAAAACCCATCA--GCATG 141
 111 PheValValProLysAsnLysAsnTyrLeuLeuLysGlnIleThrPheSerGlyProCys 130
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 142 TCTCTGCGCCAGGAGAGAATTCATGCTTGTAACTGCTCAATGCCGAGCTGATG 201
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 131 ArgSerSerIleSerValIlePheGlySerIleGluAlaSerSerLysIleSerAsp 150
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 202 CAACTCACTTAATTCTTAAAGTAGCTGGATAATGCTGCTACTAACATCTGCTTG 261
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 151 TyrLysAspArgArgLeuPheAlaPheAspSerValGlnAsnLeuValValGly 170
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 262 TGGAGAAATATGAGAAATGATGTTGCTGAGTTGCTAACTTACAGTTTACTCTA 321
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 171 GlyGlyIleAspGlyAsnGlyIleGlnValTyrProSerSerSerGlyS...-IleAsn 189
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 322 AAAGGTCTAAATGATGCTGGCAAGGAACAATGGTGGCTGCCAATGTAATGGCTCAAT 381
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 190 LysSerSerIleProCys----ArgAlaPheProThrAlaLeuThrPheThrAsnCysLys 207
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 382 GGACGGAGAAATTGCAACGATGCTGATAGACCAACGGCTTAATTCGATTTCCACG 441
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 208 AsnLeuLysValAsnAsnLeuLysSerLysAsnAlaGlnIleHisIleLysPheGlu 227
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 442 GGTCCTGATATCTTCAAGGAGCTGAACTTAACTGATCCAAATTCTTATTGATTTGG 501
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 228 SerCysThrAsnValValAlaSerAlaSerAlaLeuMetIleAsnAlaLasAlaSerAlaLysSerProAsn 247
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 502 AATGCTGAGGAGAAATCATCGCATGTTACCGACCGAGACAGCTCTAAC 561
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 248 ThrAspGlyValHisValSerAsnThrGlnTyRleGlnIleSerAspThrIleGly 267
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 562 ACTGATGGATGATGATCTTGTGCAATCTAAACTTCACTTAAAGAACAGATAGGA 621
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 268 ThrglyAspAspCysIleSerIleValSerGlySerGlnAsnValGlnAlaThrAspIle 287
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 622 ACAGGGGGAAGTCTGCTGCTATAGGCAAGCTCTTAATTTGCTATTGATGGATG 681
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 288 ThrCysGlyProGlyHsGlyIleSerIleGlySerIleGlySerGlyAsnSerGlnAla 307
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 682 ATTTGCGCTCCAGCCAGCAGTAAGTAGCTAGGAGTCTGGAGGAACACTGAGCA 741
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 308 TyrValSerAsnValThrValAsnGluAlaLysSerIleGlyValGlnAsnValAsn 327
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 742 GAGGTTCTATAGCTGCGCTGAAATGGCTTAATCTAGACACAAATGGATAGA 801
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 328 IleLysThrTrpGlnGlyIleSerGlyGlnAlaSerAsnIleLysPheLeuAlnValGlu 347
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 802 ATCAAACATGGCAGGCTGGTCTGAGGATGGAAAGCTATATTATGAGATGTTGA 861
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 861 REFERENCE/DOCKET NUMBER: 36,924
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 NAME: Carl J. Schwedler
 REGISTRATION NUMBER: 36,924
 REFERENCE/DOCKET NUMBER: CGNE 26-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEX/FAX: (916) 753-5110
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 219 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA

Alignment Scores:
 Prod. No.: 2.15e-34
 Score: 366.00
 Percent Similarity: 100.00%
 Best Local Similarity: 98.59%
 Query Match: 95.31%

Alignment Scores:	2.15e-34	Length:	219
Pred. No.:	366.00	Matches:	70
Score:	100.00%	Conservative:	1
Percent Similarity:	98.59%	Mismatches:	0
Best Local Similarity:		Total:	
Query Match:	15.31%		

DB: 1 Gaps: 0 ; TITLE OF INVENTION: ANTISENSE REGULATION OF GENE EXPRESSION
 US-10-691-374-2 (1-457) x US-09-463-213-1 (1-219) ; IN PLANT/CELLS
 QY 71 AsnGlyLleValLeAsnValLeSerPheGlyAlaLysGlyArgGlyLysThrTyr 90 ; NUMBER OF SEQUENCES: 2
 Db :: ; CURRENT APPLICATION DATA:
 7 CATGGGATTAAGTGTAACTGACTTACGTTAGCTTGAGCTAAGGTGAAACATAT 66 ; APPLICATION NUMBER: US/07/750,505
 QY 91 AsparagineLeaPheGluGlnAlaTrpAsnGlnAlaCysSerArgTh-ProValGln 110 ; FILING DATE: 27-AUG-1991.
 Db 67 GATAATATTGCAATTGAGCAACGATGATGAGCAGTTCTAGAACCTCGTCAA 126 ; PRIOR APPLICATION DATA:
 QY 111 PheValValProLysAsnTyrLeuLeuLysGlnIleThrPheSerGlyProCys 130 ; APPLICATION NUMBER: 240,408
 Db 127 TTGTGCTTCCTAAACAGAAGATTATCTCTCAAGAACATCCAGTCCATGC 186 ; FILING DATE: 30-AUG-1988
 QY 131 ArgSerSerIleSerValLeAsnValLePheGlySer 141 ; APPLICATION NUMBER: 920,574
 Db 187 AGATCTCTTTCAGTAAGATTGGATCC 219 ; FILING DATE: 17-OCT-1986
 ; SEQ ID NO:1; LENGTH: 219 ; FILING DATE: 28-MAR-1986
 RESULT 11 ; SEQ ID NO:1; LENGTH: 219 ; SEQ ID NO:1; LENGTH: 219
 5453566-1 ; ALIGNMENT SCORES:
 ; TITLE OF INVENTION: ANTISENSE REGULATION OF GENE EXPRESSION ; PRED. NO.: 2.15e-34
 ; IN PLANT/CELLS ; SCORE: 366.00
 ; CURRENT APPLICATION DATA: ; Matches: 70
 ; APPLICATION NUMBER: US/07/750,505 ; Percent Conservative: 1
 ; FILING DATE: 27-AUG-1991 ; Mismatches: 0
 ; PRIOR APPLICATION DATA: ; Indels: 0
 ; APPLICATION NUMBER: 240,408 ; Query Match: 98.59%
 ; FILING DATE: 30-AUG-1988 ; DB: 6
 ; APPLICATION NUMBER: 920,574 ; Gaps: 0
 ; FILING DATE: 17-OCT-1986 ; QY 71 AsnGlyLleValLeAsnValLeSerPheGlyAlaLysGlyArgGlyLysThrTyr 90
 ; APPLICATION NUMBER: 845,676 ; Db 7 CATGGGATTAAGTGTAACTGACTTACGTTAGCTTGAGCTAAGGTGAAACATAT 66
 ; FILING DATE: 28-MAR-1986 ; QY 91 AsparagineLeaPheGluGlnAlaTrpAsnGlnAlaCysSerArgTh-ProValGln 110
 ; SEQ ID NO:1; LENGTH: 219 ; Db 67 GATAATATTGCAATTGAGCAACGATGATGAGCAGTTCTAGAACCTCGTCAA 126
 ; ALIGNMENT SCORES: ; QY 111 PheValValProLysAsnTyrLeuLeuLysGlnIleThrPheSerGlyProCys 130
 ; PRED. NO.: 2.15e-34 ; Db 127 TTGTGCTTCCTAAACAGAAGATTATCTCTCAAGAACATCCAGTCCATGC 186
 ; SCORE: 366.00 ; QY 131 ArgSerSerIleSerValLeAsnValLePheGlySer 141
 ; PERCENT SIMILARITY: 100.00% ; Db 187 AGATCTCTTTCAGTAAGATTGGATCC 219
 ; BEST LOCAL SIMILARITY: 98.59% ; ALIGNMENT SCORES:
 ; QUERY MATCH: 15.31% ; PRED. NO.: 2.15e-34
 ; DB: 6 ; LENGTH: 219 ; SCORE: 366.00
 ; GAPS: 0 ; MATCHES: 70 ; CONSERVATIVE: 1
 ; MISMATCHES: 0 ; INDELS: 0
 ; US-10-691-374-2 (1-457) x 5453566-1 (1-219) ; US-10-691-374-2 (1-457) x 5453566-1 (1-219)
 QY 71 AsnGlyLleValLeAsnValLeSerPheGlyAlaLysGlyArgGlyLysThrTyr 90 ; TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO
 Db :: ; SEQUENCE 2998, Application US/09107532A ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 ; PATENT NO. 6583275 ; NUMBER OF SEQUENCES: 7310
 ; GENERAL INFORMATION: ; CORRESPONDENCE ADDRESS:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street ; ADDRESS: 100 Beaver Street
 ; CITY: Waltham ; CITY: Waltham
 ; STATE: Massachusetts ; STATE: Massachusetts
 ; COUNTRY: USA ; COUNTRY: USA
 ; ZIP: 024354 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-ROM ISO9660 ; COMPUTER: PC
 ; OPERATING SYSTEM: <Unknown> ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/107,532A
 ; FILING DATE: 30-Jun-1998 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/085,598 ; APPLICATION NUMBER: 60/051571
 ; FILING DATE: 14 May 1998 ; FILING DATE: JULY 2, 1997
 ; APPLICATION NUMBER: 60/051571 ; ATTORNEY/AGENT INFORMATION:
 ; WILLIAM R. KNAUF, VTC ; WILLIAM R. KNAUF, VTC

RESULT 12

5453566-1

; Patent No. 5453566

; APPLICANT: SHEWMAKER, CHRISTINE K.; KRIDL, JEAN C.; HIATT,

; WILLIAM R.; KNAUF, VIC

NAME: Ariniello, Pamela Deneke
 REGISTRATION NUMBER: 40 489
 TELECOMMUNICATION DOCKET NUMBER: GIC-012
 TELEPHONE: (781)893-5007
 FAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 2998:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1356 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANT-SENSE: NO
 ORIGINAL SOURCE:
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1..1356
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2998:
 US-09-107-532A-2998:
 Alignment Scores:
 Pred. No.: 4.06e-25
 Score: 299.00
 Percent Similarity: 45.98%
 Best Local Similarity: 27.70%
 Query Match: 12.51%
 Db: 4
 Gaps: 15
 US-10-691-374-2 (1-457) x US-09-107-532A-2998 (1-1356)
 Qy 73 IleIysValleAsnValleSerPheGlyAlaLysGlyAspGlyLysThrTyrAspAsn 92
 Db 13 AtAAATATGATGATGATTTGACATTGGCCATGTATGAT-----GAATGAAATCT 66
 Qy 93 IleAlaPheIglnIalaPasnGluAlaCysSerSerArgThrProValGlnPheAl 112
 Db 67 GAAAGATAACACAAAGCCTGATGCTGGCAAGTGACGGAGGGGACCT--GTAATT 123
 Qy 113 ValProLysAlaLysAsnTyrLeuLeuLysGlnIleThrPhserGlyProGysArgSer 132
 Db 124 GTTCAGCAGCTGAA---TTCTAACACAGCTTATTAAAGCAATGTCRACT 179
 Qy 133 Ser-IleSerValleVallePheGlySerIleGluAlaSerSerLysIleSerAspTyrLy 152
 Db 180 TCATTTAACGCCAGGA----GGGTTCTGAAATTCTCTGAGATTCAAAGATATCC 233
 Qy 152 S-----AspArgAgleLeuTrp-----IleAlaPh 160
 Db 234 TGTGTTCATCAGTGGAGGAGTCATCGAAAGTTATGCTTCCCTGTATPATGC 293
 Qy 160 eAspSerValGlnAsnLeuIvalValGlyGlyGlyGlyThrIleAspGlyAsnGlyIva 180
 Db 294 TCAAATGAGAGACATCTCTGACTGGTTCGTCATAGATGGAAATGGAAA 353
 Qy 180 1TPTP-----ProSerSerCysLysIleAsnLysSerLeuPro 194
 Db 354 ATCGTGGCATACTTTGAAATGAAACGAT-----AACTCGCTTACCT-- 399
 Qy 194 SAGGAspAlaProThrAlaLauthrHerrAspCysLysAsnLeuLysValAsnAsl 214
 Db 400 -----CGTCCPAATGATGAGTGTTCATACATGTCATCGAAATCTGTGAGATAT 452
 Qy 214 IlysSerIysAlaIaLingInIleHisIleLysPheGluSerCysTrAnvalVal 234
 Db 453 TAATGATCAGTCAGTCAGGATGATGAAACCGATCTTGCAGTAAGCAAGTT 512
 Qy 234 aSerAsnLeuIleAsnIaSerAlaLysSerProAsnThraspGlyValHisValSe 254
 Db 513 TGATAACTGAGCATCTGAAACCCAGGGATTCAACAAATACAGACGAAATTGATCCAGA 572
 Qy 254 rAsnThrGlyItyrLegInileserAapThrIleGlyIthrglyAspAspCysIleSe 274
 Db 573 ATCAGCAAATGTCGATAGTAGATAATGCCATATGACCTGGAGGATGACTGTTG 632
 Qy 274 rIleValSerGlySer-----GlnAsnValGlnIalath 285
 Db 633 AACATGAGCAGGACTGAGATAAGATACTGAGTACAGTGGAAAGGATGCTTGCGAAATTCAC 692
 Qy 285 rAsnIleThrCysGlyIproGlyHis---GlyIleSerIleglySerLeuIysArgIys 304
 Db 693 AAATGCGCAGGATGTCATGACATGCGCCTGGCTGATAGAATGAACTGAGATGAGT 752
 Qy 304 nSerGluIalatYrValSerAsnValThrValAsnGluAlaLysIleIglnAlaIglnAs 324
 Db 753 T-----ATCGTAAATATACATTCATGATGATCTCCAGAAACTGATCG 800
 Qy 324 nGlyValArgIleIysThrIrpGlyIlysPheIleAspGlyIalasSerAsnIleS 344
 Db 801 AGGAATGCGATGAACTAGACGAGGGATCGTGGAAAGTATTGAGATTC 860
 Qy 344 wAsnValGluIwetGlnIaSpalysTyrProIleIleAspGlyIalasSerAsnIleS 363
 Db 861 CATAATGTCATGGATAATGAGTGTGTCATTATGAACTTTTATTCCTGG 920
 Qy 363 p-----ArgValGluProCysIleGlnGln----- 371
 Db 921 TCCGCGAGGGAAAGAACCCGATGATGCGAAAAAAACGCTTATCCGATAGTCACCGAC 980
 Qy 372 -----PheSerAlaValGlnVallyAsnValValTyrGluAsnIleLysGlyIthrSe 389
 Db 981 ACCAGCATTCAGAAGGATCATTTCGAAATATCACGCCAAGGAACTCCATGCTCTGC 1040
 Qy 389 x 389
 Db 1041 A 1041
 RESULT 14
 US-09-614-221A-573
 Sequence 573, Application US/09614221A
 Patent No. 6723837
 GENERAL INFORMATION:
 APPLICANT: Kartunandaa, Balasulojini
 APPLICANT: Yu, Jaehyuk
 APPLICANT: Kishore, Ganesh M.
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
 WITH STEROL SYNTHESIS AND METABOLISM
 FILE REFERENCE: 16516_075
 CURRENT APPLICATION NUMBER: US/09-614-221A
 CURRENT FILING DATE: 2000-07-12
 PRIOR APPLICATION NUMBER: US 60/142,981
 PRIOR FILING DATE: 1999-07-12
 NUMBER OF SEQ ID NOS: 626
 SEQ ID NO 573
 LENGTH: 1086
 TYPE: DNA
 ORGANISM: Saccharomyces cerevisiae
 US-09-614-221A-573
 Alignment Scores:
 Pred. No.: 6.37e-25
 Score: 296.00
 Percent Similarity: 44.85%
 Best Local Similarity: 29.55%
 Query Match: 12.38%
 Db: 4
 Gaps: 17
 US-10-691-374-2 (1-457) x US-09-614-221A-573 (1-1086)
 Qy 61 SerAsnAsnIleAspIysValAspIysAsnGlyIleIysValleAsnValleSer 80
 Db 97 TCTTGTGTCCTACMTCACCGGAAATAGTAGCAGCAGCTGTTAAAGACTTA 156
 Qy 81 PheGlyAlaLysIysAspIysAspIysThrTyrAspAsnIleIaPheIglnIalaPasn 100

Db 157 GRCGCCAGCT-----GGCAGACTTAACTGCGTTA----- 192 ; Sequence 1, Application US/09787583
 Qy 101 GluAlaCysSerSerArgThrProValGlnPheValValProLysAlanylAsnThrLeu 120 ; Parent No. 6602695
 Db -----AspCAGTGCTTACATCTGCTTACGTTGAGCACCCATTAGTCAGACAG 243 ; GENERAL INFORMATION:
 Qy 121 LeuLeuGlnLeuLeuThrPheSerLeuProCysArgSerSerIleSerValValLeu 140 ; APPLICANT: DSM N.V.
 Db -----GAATGGAGCCGCTTA-----ATTCATACT----- 270 ; APPLICANT: France, Maartje
 Qy 141 SerLeuGluAlaSerSerIleLeuSerAspThrLysAspArgAspLeuPheLeu 160 ; APPLICANT: Grassin, Catherine
 Db -----TCAGGGCTTAATTCAG----- 271 ; APPLICANT: Herweijer, Margaretha
 Qy 161 AspSerValGlnAlaLeuValValGlyGlyGlyGly-----ThrIleAlanylAsnGlyGln 179 ; APPLICANT: Meeuwen, Petrus
 Db 289 -----GTTGTTGCTTCGGCATACATGATGCGAGGCA 330 ; APPLICANT: Ooijen, Albert
 Qy 180 ValItrPrpPrpProSerSerCysPheIleAsnIleSerLeuProCysArgAspAlaProThr 199 ; APPLICANT: Voragen, Alphonse
 Db 331 AATGTGGATGGCTTAGGGATAGCGGTAAAGTCKAACCC-----AGTGTAAAGTG 387 ; TITLE OF INVENTION: ASPERGILLUS TUBIGENSIS POLYGALACTURONASE
 Qy 200 AlaLeuThrPheTrpAsnCysIleAsnLeuLeuValAlaLeuLeuIleAspLeu 219 ; FILE REFERENCE: 24615-20144-00
 Db 388 GCGTTAACG-----GGAACATCTTAAGTCACCGATTGAAATTAAATGCT 435 ; CURRENT APPLICATION NUMBER: US/09/787, 583
 Qy 220 GlnGlnIleHisIleLeuPheGluSerCysThrAsnValValAlaSerAlaLeuMetIle 239 ; CURRENT FILING DATE: 2001-03-19
 Db 436 CCGCACCAAGCTTCAGCATCAAATGTCAGTTAACATCCGCAATACATT 495 ; PRIORITY NUMBER: EP 98203171. 8
 Qy 240 AspAla-----SerAlaLeuSerProAsnThrIleAspGlyIleValIleAsn 255 ; PRIORITY FILING DATE: 1998-09-18
 Db 496 GATPATCAGAGCCGGTGTCTGCCTGGGTCTAAATACGGTGGTTGATGTGGTGT 555 ; NUMBER OF SEQ ID NOS: 2
 Qy 256 ThrlGlnIleLeuIleSerAspThrIleIleGlyIleGlyAspAspCysIleSerIle 275 ; SOFTWARE: FastSEQ for Windows Version 4.0
 Db 556 TCTTAGTAACTGCTTAATCTAACGGATGACTGTTATATCGGGATGACTGATTGCTG 615 ; LENGTH: 1570
 Qy 276 ValSerGlySerGlnAlaValGlnAlaThrAlaLeuIleThrCysGlyProGlyHisGlyIle 295 ; SEQ ID NO: 1
 Db 616 ATTCCCGCTTC-----ACTATTAATTTGACAACATCTACATGGCATGTTATT 672 ; LENGTH: 1570
 Qy 673 TCTGTAGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAA 729 ; ORGANISM: Aspergillus tubingensis
 Db 316 GluAlaIleLeuIleGlyAlaLeuIleGlyIleGlyIleGlyIleGlyIle 335 ; FEATURE: CDS
 Db 730 ATTAACCATGTGTTCACTCTGCAACAGGGTGAGATAAAACCTGTAAGGTGCA 789 ; LOCATION: (172) .. (1260)
 Qy 296 SerIleGlySerIleLeuIleGlyIleAsnSerGluAlaIleThrIleAsnSerIle 315 ; PRED. NO.: US-09-787-583-1
 Db 673 TCTGTAGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAA 729 ; ALIGNMENT SCORES:
 Qy 516 ATTCCCGCTTC-----ACTATTAATTTGACAACATCTACATGGCATGTTATT 672 ; Pred. No.: 2.33e-24
 Db 475 GGTGCGCAGAGCTCACTCGAGGGTGTGGCTGGCTGAGCGCAAGGGTGGACGGTGGC 534 ; Length: 1570
 Qy 673 TCTGTAGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAA 729 ; Matches: 81
 Db 535 AGACGCCAGCCAAAGTTCTCCAGGICCAG----- 567 ; Conservative: 59
 Query Match: 12.28% ; Mismatches: 96
 DB: 4 ; Indels: 41
 Gaps: 14

US-10-691-374-2 (1-457) x US-09-787-583-1 (1-1570)

Qy 171 GLYGLYIleAsnGlyAsnGlyGlyGlnValItrPrp----- 182 ;
 Db 475 GGTGCGCAGAGCTCACTCGAGGGTGTGGCTGGCTGAGCGCAAGGGTGGACGGTGGC 534 ;
 Qy 183 -----ProSerSerCysPheIleAsnIleSerLeuProCysArgAspAlaProThr 199 ;
 Db 535 AGACGCCAGCCAAAGTTCTCCAGGICCAG----- 567 ;
 Qy 200 AlaLeuThrPheTrpAsnCysIleAsnLeuLeuValAlaLeuLeuIleAspSerIleAla 219 ;
 Db 568 ---CTCGACGAGTCCAGCATCAGCGCTGAGATCTACAAACCCCTGTCAGGGCTTC 624 ;
 Qy 220 GlnGlnIle-----HisIleLeuPheGluSerCysThrAlaValValAlaSerAlaLeu 237 ;
 Db 625 AGCATCTGGTGGACACC-----ACCATCACTGACCATGACAATCC 675 ;
 Qy 238 MetIleAlaSerAlaLeuSerProAsnThrIleAspGlyIleValIleAsnThrGln 257 ;
 Db 676 GCC-----GGTACGAGCAAGGCCAACACCGATGCCCTTGACATGGTCAGAGTAC 729 ;
 Qy 258 TyrIleGlnIleSerSerPheIleIleGlyIleAspAspCysIleSerIleValSer 277 ;
 Db 730 TACATCCACGCGACGGTGCACCGCTACACCGAGATGATGCTGGCCATCRACTCG 789 ;
 Qy 392 LysValAlaIleLeuPheAspCysSerThrAlaProCysIleGlyIleLeuIleMet 410 ;
 Db 850 ATTGTATCAGAGCGGATTTGTAATGATG-----AAGACTACTGGAACTGCTACAGGTGGC 906 ;
 Qy 375 ValGlnAlaIleLeuIleAsnIleLeuIleGly-----ThrSerAlaThr 391 ;
 Db 907 GTCGCCATTTCGCAATTGATGATGAGGATACCGGGAGCGTGACTCCACAGGAAG 966 ;
 Qy 392 LysValAlaIleLeuPheAspCysSerThrAlaProCysIleGlyIleLeuIleMet 410 ;
 Db 967 AGGGTTAAATTTGTTGGAGAAACGCTACTACTGCAATGCTGCTGCTGCTGCTGCT 1026 ;
 Qy 411 GluAsnIleAsnLeuIleValGlyIleAspPro-----SerGluAlaThrCys 427 ;
 Db 1027 GGTGGCTCTCTCTTCTGAGCTCTGAGATCCCATCTGGATCTGGCTGCAAGCTG 1083 ;
 Qy 318 IleSerIleGlyAlaGlnIleArgIleLeuThrItrPheGlyIleSerGlyGln 337 ;
 RESULT 15
 US-09-787-583-1

Db 904 AAGGTGCTRACTCCAGAACGGGTCGGTATCAAGACCATCTACGGCAGACCGGACT 963
Qy 338 AlaserAsnIleLysPheLeuAsnValIleMetGlnAspVal---LysTrpProIle 356
Db 964 GTTGAGAGAGTCAGTCAGGACATCACCCCTTCGAGCATAGCAGTAGGTATCGTC 1023
Qy 357 IleAspGlnAsnTyrCysAspArgValGluProCysIleGlnPheSerIleAlaValGln 376
Db 1024 GTTGAGAGAGACAC--GAGAACGGCAGCCCACGGCACCCCCACAAACGGTGTCAG 1080
Qy 377 ValIysAsnValValTyrGluAsnIleIysGly-----ThrSerAlaThrIysVal 393
Db 1081 GTTGAGAGACATCACTTCAGAGGTACCCAGGCTCACCGCAGGCTCAGAGCTGCTGTTACTGACATC 1140
Qy 394 AlaaIleLysPheAspCysSerIleAsnProCysIleGlyIleIleMetGluAsnIle 413
Db 1141 TACATCCTG----TGCGGTTCCGC--AGCTGCTCGACTGACCTGAGGGTGT 1191
Qy 414 AsnLeuIvalGlyGluSerGlyLysProSerGluIalThrCysLysAsnVal 430
Db 1192 GAGTGACCCGGC----GCGAGAGAC--AGCAAGTGCAAGAAGCTC 1233

Search completed: March 5, 2005, 02:29:24
Job time : 251 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: March 4, 2005, 12:45:39 ; Search time 640 Seconds
(without alignments)
4227.065 Million cell updates/sec

Title: US-10-691-374-2

Perfect score: 2390

Sequence: 1 MVIGRNSILLIIFASSIS.....VTPHCTSLBISEDBALLNY 457

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Command line parameters:
-MODE:frame+P2N.model -DEV=xLP
-DB=/cgn2.1/USP/TO/spool/p/USI0691374/runat_28022005_120705_20976/app/query.fasta_1.647
-Q=0 -OPENP=0 -UNIPR=bits -START1=1-BND=1-MATRIX=blosum62-TRANS=human40.cdi
-LIST=15 -DOCALGN=200 -THR SCOR=PCP -THR MAX=100 -THR MIN=0 -ALIGN=15
-MOD=local -OUT=mpio -HEAPSZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=USI0691374 @CGN_1_1_708@runat_28022005_120705_20976 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=20 -WARN TIMEOUT=0 -THREADS=1 -XGAPEXT=0 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N GeneSeq_16Dec04:*

1: geneseqn1980:*

2: geneseqn1998:*

3: geneseqn2008:*

4: geneseqn2001ab:*

5: geneseqn2001bb:*

6: geneseqn2002ab:*

7: geneseqn2002bb:*

8: geneseqn2003ab:*

9: geneseqn2003bb:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004ab:*

13: geneseqn2004bb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description

1	2390	100.0	1624	1 AAN9112
2	2390	100.0	1636	2 AAG38415
3	2390	100.0	1636	4 AAC04653
4	2390	100.0	1637	1 AAN0487
5	1820	76.2	5822	6 AAS20853

RESULT 1
AAN9112
ID AAN9112 standard; DNA; 1624 BP.
XX
AC AAN9112;
XX
DT 25-MAR-2003 (revised)
DT 21-JUN-1990 (first entry)
XX
DB Polygalacturonate (PG) gene cDNA.
XX
KW Polygalacturonase gene; tomato; ds.
XX
OS Lycopersicon esculentum.
XX
FH Location/Qualifiers
FT 47..1418
FT CDS /*tag= a
XX
PN US4801540-A.
XX
PP 31-JAN-1989.
XX
PR 02-JAN-1987; 87US-00000201.
XX
PR 28-MAR-1985; 86US-00846676.
PR 17-OCT-1986; 86US-00920574.
XX
PA (CALJ) CALGENE INC.

	1371	CACGCACTTCACTAGAATTCAGAGGATGAGCTTGTATTAT	1421
RESULT	4		
ID	AAN80487	standard; DNA; 1637 BP.	
XX			
AC	AAN80487;		
DT	25-MAR-2003	(revised)	
DT	20-NOV-1990	(first entry)	
DE	Plasmid clone pProm6.		
XX			
KW	Fruit ripening; polygalacturonase; pectin esterase; ss.		
OS	Synthetic.		
XX			
PH	Location/Qualifiers		
CDS	51..1424		
PT	/tag=a		
PT	/label=polygalacturonase		
XX			
PH	key		
EP271988-A.			
XX			
PD	22-JUN-1988.		
PF	06-NOV-1987; 87EP-00309853.		
PR	11-NOV-1985; 86GB-00026079.		
PA	(ICIL) IMPERIAL CHEM IND PLC.		
PA	(ZENE) ZENICA LTD.		
PI	Bridges RG, Schuch WW, Grierson D;		
XX			
XX	WPI: 1988-169271/25.		
DR	P-PSB; AAP80299.		
XX			
PT	Recombinant DNA comprising promoter and terminator sequences - useful in plants for altering ripening properties esp. in tomatoes.		
XX			
PS	Disclosure; Page 2; 22pp; English.		
XX			
CC	This cDNA clone, encoding polygalacturonase (PG), is used to produce antisense mRNA (with an inverted sequence to that of PG mRNA) which is inserted into a vector used to transform plants which thereafter have altered ripening properties. The inverted sequence and the PG mRNA form a double-stranded structure which inhibits expression of the PG mRNA. See also AAN80488. (Updated on 25-MAR-2003 to correct PA field.)		
CC	sequence 1637 BP; 598 A; 232 C; 290 G; 517 T; 0 U; 0 Other;		
SQ	Alignment scores:		
Pred. No.:	6.09e-219	Length:	1637
Score:	2390.00	Matches:	457
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0
US-10-691-374-2 (1-457) x AAN80487 (1-1637)			
QY	1 MetValIleGlnArgAsnSerIleLeuLeuLeuLeuLeuPheAlaSerIleSerIleSerIle 20		
Db	51 ATGGTTATCCAAAGGAATGATTCCTTCATTAATTTGCTTCATCATTC 110		
QY	21 ThrCysArgSerAsnValIleLeuAspSerAsnLeuPhySglValTYAspAlaIleIle 40		
Db	111 ACTTGAGCAGCATGTTGATGACATTTCAACAAGTTTATGATAATATCT 170		
QY	41 GluGluIleAlaAspPheGlnAlaTyroLeuSerTyroLeuSerIleAspGlnAsn 60		
DB:			
QY	61 SerAsnAsnAsnIleAspIysValAspIysValAspGlyIleIysValIleAlaValLeuSer 80		
Db	231 AGCARCAAATATGACAGGTGATAAAATGGATTAAAGTGTAAATGTACTTGC 290		
QY	81 PheGlyIalIysGlyIysPheGlyIysThrPheAspAlaLeuPheGluGlnAlaPhe 100		
Db	291 TTGGCGACTTGGGTGATGAGAACATAGATAATTCGATTGAGCAGCATGGAAT 350		
QY	101 GluIalaCysSerSerSerArgThrProValGlnPheValValProLysAlaLysTrpIle 120		
Db	411 CTCAAGCATAATCACTTTTCAGGTCATGGCATGAGTCATCTCTTATTCGTAAGTTGGA 470		
QY	141 SerIeuglIalaSerSerIleSerAspDtyIysAspArgAspGlyLeuPheAlaPhe 160		
Db	471 TCCTTGAAGCATCTGAAATAGTCAGACTTCATTTGGTCCTAAACAGGATTC 530		
QY	161 AspSerValGlnAsnLeuValValGlyGlyGlyThriIeasGlyIysGlyIysGly 180		
Db	531 GATAGTGTCAAAATTAGTCAGACTTCATTTGGAGGAGGACTTCATGGCATGGAGTA 590		
QY	181 TrpTrpProSerSerCysBlysIleAsnIysSerIeuproCysSerGlyAspAlaProThrAla 200		
Db	591 TGGTGGCCAAAGTCCTGCAATAATAATAATAATACTACGCCATGGATGCCAAAGGCC 650		
QY	201 LeuIhrPheTrpAsnCysIlysValAsnLeuIysValAsnAsnLeuIysSerIysAsnIys 220		
Db	651 TAACTTCGGAATTCGAAATTGTCATGTCATGTTGACATGTTGACCTTCATGAACTTCAATTTGCAATGAGTA 770		
QY	711 CAATACTCATCAATTCGACATGTCATGTCATGTTGACATGTTGACCTTCATGAACTTCAATTTGCAATGAGTA 770		
Db	241 AlAserAlaIysSerProAsnThrAspGlyValIysValAsnSerAsnThrGlyIysIleGln 260		
Db	771 GCTTCAGCAAGAGCCAAATACTCATGTTGACATGTCATGAACTTCAATTTGCAATTTCA 830		
QY	261 IleSerAspThrIleIleGlyIysCysIysAspPheSerIleSerIleIleValSerIysAsnIys 280		
Db	831 ATATCTGAACTATTATGGACAGGTGATGTTCAATGTTCTGGATCTCA 890		
QY	281 AsnValGlnAlaIthAsnIleThrCysGlyIysProGlyIysGlyIysSerIleGlyIysIle 300		
Db	891 ATATGCGAGCCACAAATATCTGTTGGTCAGGTCTATGTCATGTTGACATGTTGAGCTA 950		
QY	301 GlySerGlyAsnSerGluIaItyValSerAsnValThrValAsnGluIaItyIleIle 320		
Db	951 GCGATCTGGAAATTCAGAACTTATGTCATGTCATGTCATGAACTTCAATTTAC 1010		
QY	321 GlyIalGluIaItyValArgIleIysThrIrgGlyIysSerIysGlnAlaSerI 340		
Db	1011 GGTGCGGAAATGGACTTACGATCAAGCTGGAGGAGTCGGACAGCTGACAC 1070		
QY	341 IleValPheLeuAsnValGluMetGlnAspValIleIysValAlalleIysPheAspCysSer 360		
Db	1071 ATCAATTCCTGTAATGTTGAAATGAGCTTGTATCCATTTATGACCAAC 1130		
QY	361 TTYCysAspGlyValGluIysCysIleGlnIysValIysValIysValIys 380		
Db	1131 TATTCGATGTCAGTTCGACCATGATACAACTGAGTTTCAGGTCAGTCAGTCAGAAATGTC 1190		
QY	381 ValIysGluIleIysGlyIysSerIleIysValIysValIysValIysValIys 400		
Db	1191 GTGATGAGATACAGGCAACAGTGCACAAAGTGCCTAAATTGATGTCAG 1250		
QY	401 ThrasPheProCysGluIysIleIleMetGluAsnIleLeuValGlyIysSerIys 420		
Db	1251 ACACACTTCATGTCAGGCAATATAATGGAGATATAATTAGGGAGAATGGA 1310		

Qy 421 LysProSerGluAlaThrCysLysAsnValHisPheAsnAsnAlaGluHisValThrPro 440
 Db 1311 AACCATCGAGGTCTACGTGCCAAATGTCATTAAATGGTACATGTCAGTGACATCACCA 1370
 Qy 441 HisCysThrSerLeuGluLysSerGluAlaGluAlaLeuLeuThrAspTyr 457
 RESULT 5
 AAS20853
 ID AAS20853 standard; DNA: 5822 BP.
 XX
 AC AAS20853;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DB Expression cassette, pFP-IRNL useful for gene silencing.
 XX
 KW Inhibition of gene expression; expression cassette; inverted repeat; IR;
 NOS; noseline synthase; figwort mosaic virus promoter; FMV; hsp70; PG;
 plant heat shock 70; tomato; polygalacturonase; disease resistance;
 flavour; nutritional characteristic; plant; gene silencing; pFP-IRNL;
 regulating gene expression; mutant; ds.
 XX
 OS Lycopersicon esculentum.
 OS *Aerobacterium tumefaciens*.
 OS Figwort mosaic virus.
 OS Synthetic.
 OS Chimeric.
 XX
 PN WO200214472-A2.
 XX
 PD 21-FEB-2002.
 XX
 PR 14-AUG-2001; 2001WO-US025538.
 XX
 PR 15-AUG-2000; 2000US-0225508P.
 PR 07-AUG-2001; 2001US-00924197.
 XX
 PA (DNAP) DNA PLANT TECHNOLOGY CORP.
 XX
 PT Guttersson N, Oeller P;
 DR XX
 DR WPI; 2002-257599/30.
 PT Reducing the expression of a target gene in a cell, comprises expressing
 PT in the cell an expression cassette comprising a promoter operably linked
 to a sense or antisense targeting sequence and an inverted repeat of a
 nopaline synthase gene.
 XX
 PS Claim 51; Page 37-39; 39pp; English.

The present invention relates to an improved method for inhibiting the expression of a target gene in a cell, by expressing in the cell an antisense targeting sequence having substantial identity to a subsequence of the target gene, and an inverted repeat (IR) of a subsequence of a NOS (noseline synthase) gene, where the IR is unrelated to the targeting sequence. The expression cassette, pFP-IRNL is constructed using a figwort mosaic virus (FMV) promoter in which the 5'-untranslated leader (5'-UTR) is derived from a plant heat shock 70 (hsp70) gene, the tomato polygalacturonase (PG) gene and an IR of the terminator of the Agrobacterium tumefaciens NOS gene. The method is useful for regulating expression of endogenous genes and transgenes, e.g. to regulate plant phenotypes such as disease resistance, flavour, protein or nutritional characteristics. The improved gene effect of regulating gene expression of a selected endogenous gene or transgene. The method is simple and rapid, and is suitable for high-throughput studies. Multiple transgenic constructs all containing the same repeat element can be silenced at the same time, since the initial silencing trigger mediated through the inverted repeat region will apply

CC to all of the transcripts. The present sequence represents the expression cassette, pFP-IRNL

XX

SQ Sequence 5822 BP; 1689 A; 1275 C; 1292 G; 1566 T; 0 U; 0 Other;

Db Alignment Scores:
 Pred. No.: 1.49e-163
 Score: 1830.00
 Percent Similarity: 100.00%
 Best Local Similarity: 99.71%
 Query Match: 76.15%
 DB: 6
 Gaps: 0

US-10-691-374-2 (1-457) x AAS20853 (1-5822)

Qy 112 ValValProLysAsnLysAsnThrIleLeuLysGlnIleThrPheSerGlyProCysArg 131
 Db 1387 ATGGTTCTAAACAGAAGTATCTCTTAAGCAATACCTTCAGTCAGCAGA 1446
 Qy 132 SerSerIleSerVallysIlePheGlySerLeuGluAlaSerSerIleSerAspTyr 151
 Db 1447 TCTCTTATTCAGTAAAGATTTGGATCTTAGAGCATCTGAATTCAGCTAC 1506
 Qy 152 LysAspArgArgLeuPheAspSerValGlnIleValValGlyGly 171
 Db 1507 AAAGATGAAAGCTTGGATTGATGTTGAGTGTCAAATTAGTTGTTGGAGGGA 1566
 Qy 172 GlyThrIleAsnGlyAsnGlyGlyGlnValTrpTrpProSerSerCysLysIleAsnSer 191
 Db 1567 GCAACTCATGGCAATGGACAAGTAGTGGTGGCAACTTCTGCATAATAATAATCA 1626
 Qy 192 IleuProCysArgAspAlaIotonalaluthPheTrpAspCysLysAsnLeuVal 211
 Db 1627 CTGCGATCTGAGGGATGCAACAGGCTTAACCTTCUGGAATGCAAAATTGAGATG 1686
 Qy 212 AsnAsnLeuLysSerLysAsnAlaGlnIleHisIleLysPheGluSerCysteAsn 231
 Db 1687 AATAACTCTAAAGACTAAATGCAACAACTCATTCATAATTGAGTCATGACTAAT 1746
 Qy 232 ValValAlaSerAlaLeuMetIleAsnAlaSerAlaLysSerProSerSerAspGlyVal 251
 Db 1747 GTGTTAGCTCAATTGATGATCTCTGCGAAAGCCAAATACATGATGAGTC 1805
 Qy 252 HisValSerAsnThrGlnItyIleGlnIleSerAspThrIleLeuGlyAsp 271
 Db 1807 CAGTGTAAATCTCATAATCTCATAATCTGATACTATGATGAGTCAGGGATGAT 1866
 Qy 272 CysIleSerIleLeuValSerGlySerGlnAsnValGlnAlaThrAsnIleThrCysGlyPro 291
 Db 1867 TGTTTCAATTGTTGCTCAATATGCGGGCACAATATTCTGGTCA 1926
 Qy 232 GlyHisGlyIleSerIleGlySerIleGlySerGlyAsnSerGluAlaValSerAsn 311
 Db 1927 GGTCTATGTTAGTATGTTGAGCTCAATATGCGGGCACAATATTCTGGTCA 1986
 Qy 312 ValThrValAlaGluLysAlaLeuIleGlyValGluAspGlyValArgIleLeuThrP 331
 Db 1967 GTTACCTGTAATGAAAGCCAAATATGCGGGCACAATATTCTGGTCA 2046
 Qy 332 GluGlyGlySerGluAlaSerAsnIlePheLeuAsnValGluMetGlnAspVal 351
 Db 2047 CAGGGAGGCTGGACACTAGCACTCAATTCTGAACTGGAAATGGAGAGTT 2106
 Qy 352 LysTyrProIleIleLeuAspGlnAspTyrCysAspArgValGluProCysIleGln 371
 Db 2107 AAGTATCCCTAAATATGACCAACACTTGTGATGATGAGCATTACACAG 2166
 Qy 372 PheSerAlaValGlnValAsnValValTyrGluAlaIleLysGlySerAlaThr 391
 Db 2167 TTTCAGCTTCAGTAAATGTTGATGAGATATCAAGGGCAAGTCAACCA 2226
 Qy 392 LysValAlaIleLysPheAspCysSerThrAsnPhProCysGlyIleIleMetGlu 411

QY 234 AlaSerLysLeuMetIleAsnAlaSerAlaLysSerProAsnThrAspGlyValHisVal 253 PR 06-APR-1999; 99US-0128234P.
 Db 682 GTTGTAGTAATGTTAGATCACTGCTCCGGCGATAGTCACACAGTGATTCATC 741 PR 08-APR-1999; 99US-0128714P.
 QY 254 SerAsnThrGlyLysGlyLysGlyLysSerAspThrIleLeuGlyThrGlyAspPheSerle 273 PR 16-APR-1999; 99US-0129445P.
 Db 742 ACTAACTACTCACAAACATTCGAGCTCCACTCAGATATCGAACAGGATGATGATGATA 801 PR 19-APR-1999; 99US-0130077P.
 QY 274 SerLeuValSerGlySerGlnAlaValGlnAlaThrAsnIleThrCysGlyProGlyHis 293 PR 21-APR-1999; 99US-0130499P.
 Db 802 TCCATTGAGGATCGAACGCCAAATCTTCATACTTGCATTACTGGGCCGGTCAC 861 PR 23-APR-1999; 99US-0130510P.
 QY 294 GlyLeuSerIleGlySerLeuGlySerGlyAsnSerGluLysValSerAsnValThr 313 PR 28-APR-1999; 99US-0131449P.
 Db 862 GGATCAGCATGGAGCTTGGGGACACAAATCGAACAGCTATGCTGAGCTGGAAAT 921 PR 30-APR-1999; 99US-0132487P.
 QY 314 ValAsnGluAlaLysSerIleGlyIleGluAsnGlyValArgLeuSerThrArgInly 333 PR 30-APR-1999; 99US-0132456P.
 Db 922 GTCGATGGCTGAGTCTCTGAGAGCTGACAAATGGATGTTACTGGGCCGGTCAC 981 PR 04-MAY-1999; 99US-0132484P.
 QY 334 GlySerGlyLysSerIleGlySerGlyAsnSerGluLysValSerAsnValThr 313 PR 05-MAY-1999; 99US-0132485P.
 Db 862 GGATCAGCATGGAGCTTGGGGACACAAATCGAACAGCTATGCTGAGCTGGAAAT 921 PR 06-MAY-1999; 99US-0132486P.
 QY 982 GGATCAGCACTGCCAACAACTTAATTCATAATTCGATGTTGAAACCTCAAGAAT 1041 PR 07-MAY-1999; 99US-0132487P.
 Db 1099 GCGATGCGAGTGAAGAACGTTGTGACAGAACATCTGTGAGCGAGC3TAGGATG 1158 PR 11-MAY-1999; 99US-0134541P.
 QY 354 ProIleLeuIleAspGlnAsnTyrCysAspArgValGluProCysIleGlnGlnPheSer 373 PR 14-MAY-1999; 99US-0134542P.
 Db 1042 CGCATCATATCGAACAGGAATCTGCACAGG-GACAATGGGAAAGCTATGCTCGGAATAT 1098 PR 14-MAY-1999; 99US-0134543P.
 QY 374 AlaValGlnValAsnValValTyrGluAsnIleLysGlyThrSerAlaThrIleVal 393 PR 18-MAY-1999; 99US-0134544P.
 Db 1159 GCGATAACGTGATTSCAGCGAGACTATCCATGTCAGGATTTGCTGTGAGCTGAAGAT 1218 PR 19-MAY-1999; 99US-0134545P.
 QY 414 AsnLeuValGlyGluSerGlySerGlyAsnValValIleMetGluAsnIle 413 PR 20-MAY-1999; 99US-0135124P.
 Db 1219 AAAATAAAGGA-----GGACAGCTCTTGCAAATGCAATGTTAA 1263 PR 21-MAY-1999; 99US-0135353P.
 QY 434 AsnAlaGluIleValThrProHisCySThr 443 PR 24-MAY-1999; 99US-0135629P.
 Db 1264 AACCAAGGCCCGCTTCCTAAATGCTC 1293 PR 25-MAY-1999; 99US-0136021P.
 RESULT 8 PR 27-MAY-1999; 99US-0136392P.
 AAC46786 standard; DNA; 1393 BP. PR 28-MAY-1999; 99US-0136782P.
 AC AAC46786; PR 01-JUN-1999; 99US-0137222P.
 XX DT 18-OCT-2000 (first entry) PR 03-JUN-1999; 99US-0137528P.
 XX DB Arabidopsis thaliana DNA fragment SEQ ID NO: 51398. PR 04-JUN-1999; 99US-0137530P.
 KW Hybridization assay; genetic mapping; gene expression control; PR 05-JUN-1999; 99US-0137724P.
 KW protein identification; signal transduction pathway; metabolic pathway; PR 07-JUN-1999; 99US-0137725P.
 KW promoter; termination sequence; ss. PR 08-JUN-1999; 99US-0138094P.
 OS Arabidopsis thaliana. PR 10-JUN-1999; 99US-0138344P.
 XX PN EP1033405-A2. PR 11-JUN-1999; 99US-0139119P.
 XX PR 12-JUN-1999; 99US-0139455P.
 XX PR 13-JUN-1999; 99US-0139455P. PR 14-JUN-1999; 99US-0139455P.
 XX PR 15-JUN-1999; 99US-0139455P. PR 16-JUN-1999; 99US-0139455P.
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 XX PR 23-JUN-1999; 99US-0139462P. PR 24-JUN-1999; 99US-0140354P.
 XX PR 25-JUN-1999; 99US-0140354P. PR 26-JUN-1999; 99US-0140354P.
 XX PR 27-JUN-1999; 99US-0140354P. PR 28-JUN-1999; 99US-0140354P.
 XX PR 29-JUN-1999; 99US-0140354P. PR 30-JUN-1999; 99US-0141387P.
 OS PR 31-JUN-1999; 99US-0141387P. PR 01-JUL-1999; 99US-0141842P.
 XX PR 02-JUL-1999; 99US-0142154P. PR 03-JUL-1999; 99US-0142154P.
 XX PR 04-JUL-1999; 99US-0142390P. PR 05-JUL-1999; 99US-0142390P.
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 XX PR 14-JUL-1999; 99US-0142390P. PR 15-JUL-1999; 99US-0144086P.
 XX PR 16-JUL-1999; 99US-0144086P. PR 17-JUL-1999; 99US-0144086P.
 XX PR 18-JUL-1999; 99US-0144086P. PR 19-JUL-1999; 99US-0144331P.
 PR 20-JUL-1999; 99US-0144331P.

QY 95 PheGluglnAlaTrpAsnGluLacysSerSerArgThrProValGlnPheValPro 114
 :::::::::::::::::::::|||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 214 TrGTCAAGGCATGGCTGCGactTCCTCTTGCACCCATCTATGTTCTCTC 273

QY 115 LysAsnLysAsnTyryleuLeuLysGlnLeuLysSerSerIgYProCysSerSerIle 134
 :::::::::::::::::::::|||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 274 AnGGGCAAGAGATACTTCACCAAGCACATTACATATCTGCCCATGCAAAATCAGCATC 333

QY 135 SerValLysIlePheGlySerLeuGluLysSerSerIleSerAspAspTyryAspArg 154
 :::::::::::::::::::::|||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 334 ACCTTCATGATAGAGGCTACTTGGCTGGCTCTCCAAAGGGTCAATGGAGAGGA 393

QY 155 -----ArgLeuTrpIleAlaPheAspSerValGlnAsnLeuValGlyGlyGly 172
 :::::::::::::::::::::|||:|||||:|||||:|||||:|||||:|||||:
 Db 394 ACTATTAAGGCACTGGTATTGTCATGGTAAATGGCTTACTGTGCTGGGGGG 453

QY 173 ThrIleAsnGlyAsnGlyGlnValIrrIrrProSerSerCysIleSerAspAsp 192
 :::::::::::::::::::::|||:|||||:|||||:|||||:|||||:|||||:
 Db 454 ACGTGATGATGAAATGCAAGATTTGCGAAATTCCTGCAAAACGATGGAACTT 513

QY 193 ProCysBargAspAlaProThrAlaLeuThrPheTrpAsnCysLysAsnLeuLysSerIle 212
 :::::::::::::::::::::|||:|||||:|||||:|||||:|||||:|||||:
 Db 514 GCATGCACTGATCCTCAAGCCCTGACATCTACTCCGTCAATCTGAAGTGAG 573

QY 213 AsnLeuLysSerIleAsnAlaIleGlnIleHistoleuPheGluSerCysThrAsnVal 232
 :::::::::::::::::::::|||:|||||:|||||:|||||:|||||:
 Db 574 AACTrIGAAGCTACTAACACGACAACTAACATCACAATGTCAGTGGAGGATGCAAGTT 633

QY 233 ValAlaSerIleSerIleMetIleAsnAlaSerAlaLysSerProAlaThrAspGlyValHis 252
 :::::::::::::::::::::|||:|||||:|||||:|||||:
 Db 634 AGGATCTCTGGCTGACAATCACAGCACCAAGGACTAACCCAAACACGGATGATCAT 693

QY 253 ValSerAsnThrGlyIrrIleGlyIleSerAspThrIleLeuGlyThrGlyAspCys 272
 :::::::::::::::::::::|||:|||||:|||||:|||||:
 Db 694 ATCACCAGAGTAGAAAATGTCAGTGACAGGTGACATCAGACGGGGAGATGTC 753

QY 273 IleSerIleValSerGlySerGlnAsnValGlnAlaThrAsnIleIrrCysIleProGly 292
 :::::::::::::::::::::|||:|||||:|||||:
 Db 754 ATGRCGATCGAGGTGGAACTGAGACTTCATGTCAGAACATGGGTTGCGACAGAGA 813

QY 293 HisGlyIleSerIleGlySerLeuGlySerGlyAsnSerGlnAlaTyvalSerAsnVal 312
 :::::::::::::::::::::|||:|||||:|||||:
 Db 814 CACCCATCATGATGGGGACCTAGGCAATCACACTCTGAAGCTCATGTCACATGTC 873

QY 313 ThrValAsnGluAlaValIleGlyIleGlyIleGlyAsnGlyValArgIleIrrThrTrpIle 332
 :::::::::::::::::::::|||:|||||:|||||:
 Db 874 ACCATCGGCACTGTCAGGCTATGGCACACCAACCGAGCTGCGATCAACATCGCAG 933

QY 333 GlyGlySerGlyGlnAlaSerIleIleIlePheLeuAsnValGlnAspPralys 352
 :::::::::::::::::::::|||:|||||:|||||:
 Db 934 GGRGGTCGGGGTAGCGCAAGTACATGTTTCCAGACACATGTCGGAAATGTTGG 993

QY 353 TyrProIleIleAspGlnAlaSerIleIlePheLeuAsnValGlnAspPralys 352
 :::::::::::::::::::::|||:|||||:|||||:
 Db 994 AACCCCGCTATATGCAAACTGCTACTCTGCAACACCAGCAGAACAGTRG 1053

QY 369 -----LeuIleGlnPheSerAla 374
 :::::::::::::::::::::|||:|||||:
 Db 1054 TCCATTTGTGATAATATGGAACTTATATTAGTGTGTTGCTGACATCTGCA 1113

QY 375 ValGlnIleLeuAsnValIlePheLeuAsnIleGlyIleSerIleAlaLysValAla 394
 :::::::::::::::::::::|||:|||||:
 Db 1114 GTTCAGATGATGCAATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1173

QY 395 IleLeuAspAspCysSerThrAsnAlaPheProGlyGlyIleIleMetGluAsnIleAsn 414
 :::::::::::::::::::::|||:|||||:
 Db 1174 ATCAAGCTGGACTGCGCAGAAATGACTTGGCCAGGTTAACCTTGATGATGTCAG 1233

QY 415 Leu--ValGlyGluSerGlyIleProSerGluAlaThrCysLysAsnValIlePheAsn 433
 :::::::::::::::::::::|||:|||||:
 Db 1234 CTCACTGTCAGGGAGGCTGGGTGATGGCGAGGAGCTGCCGAAACCGAAATGGGAG 1293

QY 434 AsnAlaGluHisIleValThrProAsn---CysThrSer 444

Db 1294 AAATCAGGACAGTTGTCACAGCCCTGAGCTCC 1329
 Search completed: March 4, 2005, 22:54:05
 Job time : 673 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
 Run on: March 4, 2005, 19:53:34 ; Search time 3526 seconds
 (without alignments)
 4933.457 Million cell updates/sec

Title: US-10-691-374-2
 Perfect score: 2390
 Sequence: 1 MVIQRNSTILLIIFASSIS..... VTPHCTSLISEDEALLYN 457

Scoring table: BLOSUM62
 Xgapop 10.0 ' xgapext 0.5
 Ygapop 10.0 ' Ygapext 0.5
 Fgapop 6.0 ' Fgapext 7.0
 Delop 6.0 ' Delect 7.0

Searched: 34239544 seqs, 19032134700 residues
 Total number of hits satisfying chosen parameters: 68479008
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:
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 -Q=con2 1.USPTO spool.p/US10691374/runat 28022005 120706 20996/app_query.fasta_1.647
 -UNITS=bitc -START1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGNS=0 -THR SCOREexact -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFILE=proto -NORM=ext -HRSPAN=50 -MINLEN=200000000
 -USER=US10691374 @CGN_1_5180@runat 28022005 120706 20996 -NCPU=6 -ICPU=3
 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=0.5 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
 1: gb_e8t1:
 2: gb_e8t2:
 3: gb_e8t3:
 4: gb_e8t4:
 5: gb_e8t5:
 6: gb_e8t6:
 7: gb_e8t7:
 8: gb_e8t8:
 9: gb_e8t9:

RESULT 1
 BM410796
 LOCUS
 DEFINITION EST85123 tomato breaker fruit Lycopersicon esculentum cDNA clone
 CIG554115 5' end, mRNA sequence.
 ACCESSION BM410796
 VERSION 1
 KEYWORDS EST
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spearmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 REFERENCE
 AUTHORS Alcalá,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A.,
 Tsai,J., Bougri,O., Kirtness,B., Utterback,T., Van Alen,S.,
 Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
 Giovannoni,J.
 TITLE Generation of ESTs from tomato fruit tissue, breaker stage (2002)
 JOURNAL Unpublished (2002)
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html
 This clone is available through the Clemson University Genomics
 Institute
 Seq primer: T3.

FEATURES
 Source 1. -797
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1347	56.4	797 4 BM410796	BM410796 EST585523
2	1343	56.2	786 4 BM412817	BM412817 EST587344
3	1321	55.3	774 4 BM413004	BM413004 EST587331
4	1292	54.1	767 4 BM412528	BM412528 EST586355
5	1282	53.6	742 4 BM413282	BM413282 EST58709
6	1278	53.5	749 4 BM413343	BM413343 EST58770
7	1220	51.0	709 2 AW442339	AW442339 EST31135
8	1220	50.7	696 2 AW442253	AW442253 EST31149
9	1192	49.9	687 2 AW442335	AW442335 EST311731

Qy 344 LeubasnvalglumetGlnaspVallysTyrProlelleleAspgrlnasTyrCys-A^s 363
 /db_xref="taxon:4081"
 /clone="cLEB354115"
 /tissue_type="Pericarp"
 /dev_stage="breaker"
 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit"
 /note="Vector: pBlueScriptSKmciadapt; Site 1: EcoRI;
 Site 2: XbaI; supplier: Boyce Thompson Institute;
 sequencing: The Institute for Genomic Research; Fruit
 were harvested at the breaker stage (first sign of
 lycopene accumulation on the blossom end of fruit). Fruit
 were cut in half and the seeds and locules were discarded
 prior to freezing the pericarp."
 ORIGIN

Alignment Scores:
 Pred. No.: 1.57e-144 length: 786 bp mRNA linear EST 22-JAN-2002
 Score: 1347.00 Matches: 261 cDNA clone cLEG354120 5', end, mRNA sequence.
 Percent Similarity: 98.50% Conservative: 1 EST.
 Best Local Similarity: 98.12% Mismatches: 3 Lycopersicon esculentum (tomato)
 Query Match: 56.36% Indels: 1
 DB: 4 Gaps: 0

RESULT 2
 US-10-691-374-2 (1-457) x BM410796 (1-797)
 Qy 104 SerSerArgThr-ProValGlnPheValValProLysAsnTyruLeuLeuLysGin 123
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 2 TCATCTGAGACACTGTGTCATTGTTGTTCTAAACAGATTAATCTTCAGCAA 61
 ||||| ||||| ||||| |||||
 Qy 124 IleThrPheSerGLYProCysSerArgSerSerLeuSerValValIlePheGlySerLysIlePhe 143
 ATCACCCATTGCGTCATCGAGCTCTCATGAGTTGACAGAA 121
 ||||| ||||| |||||
 Db 62 AGTTGTTGCGAAATTCAGCTACAGAATGAGCTTGATGTTGACCTAGAA 143
 ||||| |||||
 Qy 144 AlAspSerSerLysIleSerAspDPTYIysApaArgLeuPheAlpHeAspSerVal 163
 ||||| ||||| |||||
 Db 122 GCATCTGAGTAATTCAGCTACAGAATGAGCTTGATGTTGACCTAGTT 181
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 Qy 164 GluAsnLeuValValGlyGlyGlyGlyThrIleAsnGlyAsnGlyGlyGlyGlyGly 183
 ||||| ||||| |||||
 Db 182 CAAATTGTTAGTGTGAGGAGGAACTATCATGGCATGAGCATGAGTAGTGCGCA 241
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 Qy 184 SerSerCysAsnLysIleSerAspSerValEuroCysArgSpaApaOrnalaLeuThrPhe 203
 ||||| |||||
 Db 242 AGTTGTTGCGAAATTCAGCTACAGAATGAGCTTGATGTTGACCTAGAA 203
 ||||| |||||
 Qy 204 TrpAlaCysIleAsnLeuLysValAspAsnLeuLysSerIysAsnLagLagGlnIleHis 223
 ||||| |||||
 Db 302 TGGATTGCGAAATTCAGCTACAGAATGAGCTTGATGTTGACCTAGCTCAGCA 301
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 Qy 362 ATCRAATTGAGCTGACTGACTATGTTGACTCTCAATTGATGATCAGTCAGCA 421
 ||||| |||||
 Db 361 362 ATCRAATTGAGCTGACTGACTATGTTGACTCTCAATTGATGATCAGTCAGCA 421
 ||||| |||||
 Qy 224 IleAspSerProAspThrArgPheValIleSerAsnThrGlnIleGlnInSerAsp 263
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 Db 422 AACAGGCCAAATCATGATGGAGTCCATGATCAAACTACTCATATACTCATGAT 481
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 Qy 264 ThrIleLeuGlyThrGlyAspAspCysBileSerIleValSerGlySerGlnAsnValGin 283
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 Db 482 ACTTATTATGCGAACAGGTGAGATGCTATTCAATGTTCTGGATCACAATGTCGAG 541
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 Qy 284 AlaThrAsnIleThrCysGlyProGlyHsglyIleSerIleGlySerLeuGlySerCys 303
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 Db 542 GCCACAAATTAATCTCTGGTGCACGTCATGTTGAGTATTGCAAGCTTAGATCTCGGA 601
 ||||| |||||
 Qy 304 AsnSerGluAlaIleValSerAsnValThrValGluAlaIleAspIleLeuGlyAlaGlu 323
 ||||| |||||
 Db 602 ATTCTGAGACCTTACGTTGCTTAATGTTGAGCTTAAATGTTGAGCTTAAAT 721
 ||||| |||||
 Qy 324 AsnGlyValAlaIleValGlyLysTrpIleGlyGlySerGlyGlyAlaIleSerAsnIleLysPhe 343
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 Db 662 ATGGGAGTGTAGCAAGCTGGCAGGAGCTGGCAAGCTAGCCACATCAATT 721
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DEFINITION EST58714# tomato breaker fruit lycopersicon esculentum EST 22-JAN-2002
 cLEG354120 5', end, mRNA sequence.
 ACCESSION BM412817
 VERSION BM412817.1 GI:18264447
 SOURCE
 KEYWORDS Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum (tomato)
 TITLE
 JOURNAL
 COMMENT Unpublished (2002)
 REFERENCE
 AUTHORS Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S.,
 Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
 Giovannoni,J.
 Generation of ESTs from tomato fruit tissue, breaker stage (2002)
 Contact: CDSI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute
 Seq primer: T3.
 FEATURES
 source
 location/Qualifiers
 1..786
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA96"
 /db_xref="taxon:4081"
 /clone="cLEB354120"
 /tissue_type="Pericarp"
 /dev_stage="breaker"
 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit"
 /note="Vector: pBlueScriptSKmciadapt; Site 1: EcoRI;
 Site 2: XbaI; supplier: Boyce Thompson Institute;
 sequencing: The Institute for Genomic Research; Fruit
 were harvested at the breaker stage (first sign of
 lycopene accumulation on the blossom end of fruit). Fruit
 were cut in half and the seeds and locules were discarded
 prior to freezing the pericarp."
 ORIGIN

Alignment Scores:
 Pred. No.: 4.46e-144 length: 786 bp mRNA linear EST 22-JAN-2002
 Score: 1343.00 Matches: 257 cDNA clone cLEG354120 5', end, mRNA sequence.
 Percent Similarity: 98.09% Conservative: 0 EST.
 Best Local Similarity: 98.09% Mismatches: 5 Lycopersicon esculentum (tomato)
 Query Match: 56.19% Indels: 0
 DB: 4 Gaps: 0

RESULT 2
 US-10-691-374-2 (1-457) x BM412817 (1-786)
 Qy 95 PheGluGlnIleTpaAspGluAlaCysSerSerArgThrProValGlnPheValPro 114
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 Db 1 TTTCGCAAGCAGTGAAGAGAATGTTCTGATGACACCTGTTCAATTGTTGTTCT 60
 ||||| |||||
 Qy 115 LysAsnLysAsnTyruLeuLeuLysGlnIleThrPheSerGlyProCysArgSerSerIle 134
 ||||| |||||
 Db 61 AAAACAGAAATCTCTCAAGCAATCACCTTTCAGGCCATGCAAGATCTCTATT 120
 ||||| |||||

Qy 135 SerValysIlePheGlySerLeuGluLaserSerValysIleSerAspTyrLysAspArg 154
 Db 121 TCA G T A A G A T G T T T G A T C C T T A G A G C A T G A T A A T T C A G A C T A C C A G T A G A 180

Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics Institute: T3.
 Seq primer: T3.

FEATURES SOURCE

1. .774 /organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TM96"

/db_xref="taxon:4081"

/clone="CLEG6IN6"

/tissue_type="Pericarp"

/dev_stage="breaker"

/lab_host="SOLR"

/clone_id="tomato breaker fruit"

/note="vector: pBlueScriptsMNCUadapt; Site 1: EcoRI; Site 2: XbaI; supplier: Boyce Thompson Institute; Fruit sequencing: The Institute for Genetic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

ORIGIN

Alignment Scores:

Pred. No.: 1.52e-141 Length: 774

Score: 1321.00 Matches: 254

Percent Similarity: 98.84% Conservative: 1

Best Local Similarity: 98.45% Mismatches: 2

Query Match: 55.27% Indels: 1

DB: 4 Gaps: 0

US-10-691-374-2 (1-457) x BM413004 (1-774)

Qy 88 LysThrTyrAspAspIleAlaPheGluGluAlaTpaApgIuAlaCysSerSerAspGly 107

Db 3 AACACATATTGATAATTGTGATTGAGCAGCATGGATGAGCAGTCCTCAACA 62

Qy 108 ProValGlnPheValProLysAlaSerTyrLeuLeuLysGlnIleThrPheSer 127

Db 63 CCTGGTTAACATTGTGGTCTCTAAAAACAGATTATCTTCAGCAATCACCTTTCA 122

Qy 128 GLYProCysBargSerSerIleSerValLysIlePheGlySerLeuGluLaserSerLys 147

Db 123 GGTCCCTGAGCATCTTCTTCAATTTCAGAAAGATTTRGATCCTTAGAA 182

Qy 148 IleSerAspTyrLysAspArgArgLeuTriPheAlaPheAspSerValGlnAsnLeuVal 167

Db 183 ATTCAAGCTACAAAGCTTGTAGGGCTTGTTGCTTGTAGTCATTTGTT 242

Qy 168 ValGlyGlyGlyGlyIleAspGlyAspGlyIleValTyrTrpProSerSerAspLys 187

Db 243 GTTGGAGGAGGAGGAACTATCATGATGCAATGAGCTATGTTGCCCAAGTCTTGCAA 302

Qy 188 IleAsnLysSerLeuProCysBargAlaProThralAlaLeuIlePheTrpAspCysLys 207

Db 303 ATAAATAAACACTGCATGCAGGGATGCCAACGGCTTAACCTCTGAATGCCAA 362

Qy 208 AsnLeuIysValAsnLeuIysSerLysIleAsnIleGlnIleAspIleLysPheGlu 227

Db 363 ATTCAAGCTACAAAGCTTGTAGGGCTTGTTGCTTGTAGTCATTTGTT 422

Qy 228 SerCysThrAlaValAlaSerAlaLeuMetIleAsnAlaSerAlaSerProAsn 247

Db 423 TCATGCCTAACTGTTGAGCTCAATTGTGATCATGCTTCAGCAAGGCCAA 482

Qy 248 ThrAspGlyValIleValSerAspThrGlyIleArgIleAspPheIleGly 267

Db 483 ACTGAGGAGGCGATGATCAACTCTAAATATCTGATCATTTGAA 542

Qy 268 ThrglyAspAspCysIleSerIleValSerGlySerGlnAsnValGlnAlaThrAlaIle 287

Db 543 ACAGGTGATGTTGTTCAATTCTGCGATCTCAAATGTGCGGCCACAAATT 602

REFERENCE
 AUTHORS Alcalá, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai, J., Bouzou, O., Kitchin, B., Utterback, T., Van Allen, S., Roming, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 TITLE Generation of ESTs from tomato fruit tissue, breaker stage (2002)
 JOURNAL Unpublished (2002)
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA

		Db	543	TGGCCHAGTCTTGCAAATAATCACTGCGATGCAGGGATGCCACAGGCCCTA	602
Email:	http://www.genome.clemson.edu/orders/index.html	Qy	202	ThrPheTrpAsnCysLysBlaLeuValAsnLeuValSerLysAsnLeuValGln	221
This clone is available through the Clemson University Genomics Institute		Db	603	ACCTCTGGAAATTGCGAAATTGAAAGATTAATCTAAAGACTAAATGCGAACACA	662
Seq primer: T3					
FEATURES		Location/Qualifiers			
SOURCE	1. .742	/organism="Lycopersicon esculentum"			
		/mol-type="mRNA"			
		/cultivar="TA496"			
		/db-xref="taxon:4081"			
		/clone="OLBG63C1"			
		/tissue-type="Pericarp"			
		/dev-stage="breaker"			
		/lab-hsbc="SOIR"			
		/clone lib="tomato breaker fruit"			
		/note="vector: pBlueScriptSK+Quadpt; site 1: EcoRI;			
		Site_2: Xhol; supplier: Boyce Thompson Institute, Inc.			
		Sequencing: The Institute for Genomic Research. Fruit			
		were harvested at the breaker stage (first sign of			
		lycopene accumulation on the blossom end of fruit). Fruit			
		were cut in half and the seeds and locules were discarded			
		prior to freezing the pericarp."			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.6e-137	length:	742		
Score:	1.282.00	Matches:	246		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:		Mismatches:	0		
Query Match:	53.64%	Indels:	0		
DB:	4	Gaps:	0		
US-10-691-374-2 (1-457) x BM413282 (1-742)					
		RESULT 6			
		BM413343			
		LOCUS	BM413343		
		DEFINITION	EST58760 tomato breaker fruit Lycopersicon esculentum cDNA clone		
		CLBG63C1	5' end, mRNA sequence.		
		ACCESSION	BM413343		
		VERSION	BM413343.1		
		EST:	GI:10264973		
		KEYWORDS			
		SOURCE	Lycopersicon esculentum (tomato)		
		ORGANISM	Lycopersicon esculentum		
		Bivalvia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
		Spemaphyta; Magnoliophyta; eudicots; asterids; lamiids; Solanales; Solanace; Solanum; Lycopersicon.			
		REFERENCE	1 (bases 1 to 749)		
		Arcila,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A.,			
		Tsai,J., Bougri,O., Kirchner,E., Utterback,T., van Alen,S.,			
		Romning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and			
		Giovannoni,J.			
		TITLE	Unpublished (2002)		
		JOURNAL			
		COMMENT	Contact: CUGI		
		Clemson University Genomics Institute			
		100 Jordan Hall, Clemson, SC 29634, USA			
		Email: http://www.genome.clemson.edu/orders/index.html			
		This clone is available through the Clemson University Genomics Institute			
		Seq primer: T3.			
FEATURES		Location/Qualifiers			
SOURCE	1. .749	/organism="Lycopersicon esculentum"			
		/mol-type="mRNA"			
		/cultivar="TA496"			
		/db-xref="taxon:4081"			
		/clone="OLBG63C1"			
		/tissue-type="Pericarp"			
		/dev-stage="breaker"			
		/lab-hsbc="SOIR"			
		/clone lib="tomato breaker fruit"			
		/note="vector: pBlueScriptSK+Quadpt; site 1: EcoRI;			
		Site_2: Xhol; supplier: Boyce Thompson Institute, Inc.			
		Sequencing: The Institute for Genomic Research. Fruit			
		were harvested at the breaker stage (first sign of			
		lycopene accumulation on the blossom end of fruit). Fruit			
		were cut in half and the seeds and locules were discarded			
		prior to freezing the pericarp."			
ORIGIN					
Alignment Scores:					
Pred. No.:	1.36e-136	length:	749		
Score:	1.278.00	Matches:	248		
Percent Similarity:	99.60%	Conservative:	0		
Best Local Similarity:	99.60%	Mismatches:	1		
Query Match:	53.47%	Indels:	1		
DB:	4	Gaps:	0		
US-10-691-374-2 (1-457) x BM413343 (1-749)					
		QY	74 LysValLeuValSerPheGlyAlaLysGlyAspGlyThrTyrAspAsnIleu	93	

	Db	3 AAGGATTAATGACTTCTGGAGCTAAGGTGATGGAAACATATAATT 62	FEATURES	Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html
Qy	94 AlpheGluglnAlatrrasnguialcysSerSerArgThrProAlpHpheVal 113	source	5 prime sequence.	Location/Qualifiers
Db	63 GCATTCGACAGCTGGATGAGCAGTCATCTAGAACCTGTTCAATTGTT 122	1. -709	/clone="cLEN1819"	
Qy	114 ProlysAsnLysAsnTyrlleuLysasnLlethrheSerGlyProCysBargserSer 133	/organism="Lycopersicon esculentum"		
Db	123 CCTAAACAGATTAATCTTCAGCAATCACCTTCAGGTCATCAGCTCT 182	/mol_type="mRNA"		
Qy	134 IleSerValyllePheGlySerLeuLalaSerSerLysSerPhePtyrsar 153	/cultivar="TA896"		
Db	183 ATTCTAGTAAGATTTGGATCTTAGAGASCATCTGAATTCAGCTACAGAT 242	/db_xref="taxon:4031"		
Qy	154 ArgArgLeuTroleaPheAspSerValGlnAsnLeuValValGlyGlyGlyThr 173	/tissue_type="pericarp"		
Db	243 AGAGGCTTGGATGCTTGATAGCTGTCAAATTGCTGAGGAGGACT 302	/dev_stage="red ripe (7-20 days post-breaker)"		
Qy	174 IleAsnGlyAsnGlyGlnValTrpProSerSerCysSystleAsnlysSerLeuPro 193	/clone_libs="tomato fruit red ripe, TAMU"		
Db	303 ATCAATGCGAATGAGCAAGATGAGTGGCCGAGCTCTGCAATATACTGCA 362	/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XbaI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."		
Qy	194 CysAspAspAlaProThrAlaLeuThrPheThrPheTrPheAsnCysAsnLeuLysValAsn 213			
Db	363 TGCAGGGATGACCACAGGCCCTAACCTCTGGATTGCAAATTGAAAGTAT 422			
Qy	214 LeuLySerLysAsnLysAlaGlnLleHsileHsilePheGluSerCysThrAsnVal 233	Alignment Scores:		
Db	423 CTAAKAGTAAATGACCAACAACTCTCATCAATTGAGCT 482	Pred. No.: 6.31e-130	Length: 709	
Qy	234 AlAspAsnLeuMetIleAsnAlaSerAlaLysSerProAsnThrAspGlyValHisVal 253	Score: 1220.00	Matches: 235	
Db	483 GCTTCATTTGATGATCATGCTTCAGCAAGGCCAACTACTGAGCTATGCTGA 542	Percent Similarity: 99.58%	Conservative: 0	
Qy	254 SerAsnThrCnTrileglnIleSerAspThrIleLysGlyAspAspCysIle 273	Best Local Similarity: 99.58%	Mismatches: 1	
Db	543 TCAAACTACATCAATTCATCAATCTGATCACTATTATGGACAGTGAGATGTT 602	Query Match: 51.05%	Indels: 0	
Qy	274 SerIleValAspGlySerGlnAsnValGlnAlaThrAsnLleThrCysGlyProGlyHis 293	Gaps: 0		
Db	603 TCAATGTTCTGGATCACAATGTCAGGCCAACTACTTGCGCCAGGCTAT 662	US-10-691-374-2 (1-457) x AW441939 (1-709)		
Qy	294 GlyIleSerIleGlySerIleGlySerGlyAsnSerGluIatryValSerAsnValThr 313	219 AlaGlnGlnIleHsileLysPheGluSerCysThrAsnValValAsnSerAsnLeuMet 238		
Db	663 GGTTAAAGTATGAGCTGAACTGCTGAAATTC-GAGCTTATGCTGAAATCT 721	Score: 2	Matches: 235	
Qy	314 ValAsnGluLalaValIleIleGlyAla 322	Db	239 IleAsnAlaSerAlaSerProAsnThrAspGlyValHisValSerAsnThrGlnTrp 258	
Db	722 GTAAATGAGCCAAATTATCGTGCC 748	62 ATCATGTTTCAAGAAAGCCAAATCTGAGGATGTTCTGATATCATCTATAT 121		
RESULT 7	AW441939	Qy	259 IleGlnIleSerAspThrIleIleGlyAspAspCysIleSerIleValSerGly 278	
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LOCUS	AW441939	Db	122 ATCCAATATCTGATACATATATTGGACAGCTGATGATGATGTTTCAATTGGA 181	
DEFINITION	709 bp mRNA linear EST 18-MAY-2001	Qy	279 SerGlnAsnValGlnAlaThrAsnLleThrCysGlyProGlyHisIleSerIleGly 298	
ACCESSION	EST11335 tomato fruit red ripe, TAMU	Db	182 TTCAAMATGTCAGGCCAACAAATTCTGGTGGCCAGTCAGGTTAGATGCA 241	
VERSION	AW441939	Qy	299 SerIleGlySerGlyAsnSerGluIatryValSerAsnValThrValAsnGluLala 318	
KEYWORDS	1. (bases 1-709)	Db	242 AGCTTGGATCTGGAGATCTGAGCTT 301	
SOURCE	Lycopersicon esculentum (tomato)	Qy	319 IleIleGlyAlaGluLysGlyValArgIleLysThrTrpIleGlyGlySerGlyGlnAla 338	
ORGANISM	Lycopersicon esculentum	Db	302 ATTATGGTGGCCGAAATGGATGGTGGATCAAGCTGGAGGGAGCTGCAACCT 361	
REFERENCE	Baryonyx; Veridiplante; Streptophyta; Embryophyta; Tracheophyta; Asperids; Lamids; Solanales; Solanaceae; Solanum; Lycopersicon.	Qy	339 SerAsnIleIlePheLeuAsnValGluMetGlnAspValLysIleThrProLeuIleAsp 358	
AUTHORS	Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.B., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ann, S., Romning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.	Db	362 AGCACATCAATTCTGAGTGTGCAAGTGCAGCTTACCTTAATAGAC 421	
TITLE	Generation of cDNA from tomato fruit tissue	Qy	359 GluAsntryCysPargArgIleProLysIleGlnInPhaserAlaValGlnValBy 378	
JOURNAL	Unpublished (1999)	Db	422 CAACATCTGTCAGCTGAGCTGACCTATCAACTGTTTCACTGTCAGGAA 481	
COMMENT	Contact: CUGI	Qy	379 AsnValValTyrglAsnIleLysGlyIleSerAlaLysValAlaIleLysPheAsp 398	
Clemson University Genomics Institute	Clemson University Genomics Institute	Db	482 ATGGGGTGTATGAGAAATCAAGGCACAAAGGTGGCCATAATTGAT 541	

Db 542 TGAGCACAACTTCCATGAGGAATTATAATGGAGATAATAATTAGTAAGGAA 601
 Qy 419 SerGlySerProSerArgThrProValGlnPheValValProLysAsnValHisPheAsnAlaGluHsval 438
 Db 602 AGTGGAACATCAGAGGTACGTGCAAATGTCATTTCACAAATGCTGTT 661
 Qy 439 ThrProHisSerThrSerLeuGluIleSerGluAspGluAlaLeu 454
 Db 662 ACACCACTGCACTCACTAGAAATTCAAGGATGAGCCTTTC 709

RESULT 8 AW442253
LOCUS AW442253 696 bp mRNA linear EST 18-MAY-2001
DEFINITION EST311649 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
ORGANISM Spermato phyta; Streptophyta; Embryophyta; Tracheophyta;
KEYWORDS EST; Lycopersicon esculentum (tomato);
REFERENCE EST311649 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
AUTHORS Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
 Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., and
 Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
 Giovannoni,J.
TITLE Generation of ESTs from tomato fruit tissue
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
 Clemson University Genomics Institute
 10 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>

FEATURES
Source

1. 696 Location/Qualifiers

/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="Taxon:4081"
/clone="CLEN22G14"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/clone_id="tomato fruit red ripe, TAMU"
/notes="Vector: pBluscript SK(-); Site 1: EcoRI; Site 2:
Xhol; Supplier: Giovannoni. Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
ORIGIN

Alignment Scores:

Pred. No.: 5.16e-129 **Length:** 696
Score: 1212.00 **Matches:** 231
Percent Similarity: 100.00% **Conservative:** 0
Best Local Similarity: 100.00% **Mismatches:** 0
Query Match: 50.71% **Indels:** 0
DB: 2 **Gaps:** 0

RESULT 9 AW442235
LOCUS AW442235 687 bp mRNA linear EST 18-MAY-2001
DEFINITION EST311731 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
ORGANISM Spermato phyta; Streptophyta; Embryophyta; Tracheophyta;
KEYWORDS EST; Lycopersicon esculentum (tomato);
REFERENCE EST311731 687 bp mRNA linear EST 18-MAY-2001
AUTHORS Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
 Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., and
 Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
 Giovannoni,J.
TITLE Generation of ESTs from tomato fruit tissue
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
 Clemson University Genomics Institute
 10 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>

FEATURES
Source

1. 687 Location/Qualifiers

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/mol_type="mRNA"

Db 63 CTCAAGGAATCACCTTTCAGTCAGCAGATCTTCTATTCAAGATTGG 122
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 Db 123 TCCTTACAGAACCTACTAAATTCTGACTCACAAAGATAGAGGCCTTGGAATTGCTT 182
 Qy 161 AspSerValGlnAlaLeuValValGlyGlyGlyThrIleAsnGlyYasGlyGlnVal 180
 Db 183 GATAGCTCAAAATTAGTGTGGAGGAGGACTCATCAATGCAATGCA 242
 Qy 181 TTPTrproSerSerCysLysTleAsnlysSerLeuProCysArgAspAlaProThala 200
 Db 243 TGGGGCAAGTCCCTCCACAAATAATACCTGCATGGGGTGCAACGCC 302
 Db 363 CAATCTATCAATTAATTGACTCCACTATGCTCAATTGATGACCA 220
 Qy 241 AlaSerAlaValSerProAsnThrAspGlyValHisValSerAsnThrGlnTyroLeGln 260
 Db 423 GTTCAGCAAGAGCCAAACTCTGATGGAGTCATGTCATTAATCTATTCAA 482
 Qy 261 IleseraspThrLeuGlyValGlyAspPcylValIleserLeuValSerGlySerGln 280
 Db 483 ATATCTCTACTATTATGGACAGGATGATGTTCAATGTTCTGATCCTAA 542
 Qy 281 AarValGlnAlaThrValLeuThrCysGlyProGlyValGlyIleserIleGlySerLeu 300
 Db 543 ATATGCGAGGCCACAAATTACTTGCTCCAGGCTATGTTATAAGTATGCGACTTA 602
 Qy 301 GlySerGlyAsnSerGluAlaTyraValSerAsnValThrValAsnGluAlaValIle 320
 Db 603 GATCTGGAATTCAGAGCTATGCTTAATGCTAAATGTAATGAGCCAAATTATC 662
 Qy 321 GYAIAAGIAGAAGLYVAGIAGLYVAGIAGLYVAGIAGLYVAGIAGLY 331
 Db 663 GGTGCCAAATGGAGTAGGTCAAGACTGG 695

/db_xref="taxon:4081"
 /clone="CLBN2CL13"
 /tissue_type="pericarp"
 /dev_stage="red ripe (7-20 days post-breaker)"
 /clone_lib="tomato fruit red ripe, TAMU"
 /note="Vector: pBluscript SK(-); Site_1: EcoRI; Site_2:
 XbaI; supplier: Giovanni, Fruit were tagged at the
 breaker stage (first sign of lycopene accumulation on the
 blossom end of the fruit) and harvested 7 days
 post-breaker (fully red-ripe), 10 days post breaker, and
 20 days post-breaker (over-ripe). 20 day fruit which
 showed external or internal signs of pathogenesis were
 discarded. Fruit were cut in half and the seeds and
 locules were discarded prior to freezing the pericarp."

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-691-374-2 (1-457) x AW442335 (1-687)

Qy

76

IleAsnValLeuSerPheGlyAlaLysGlyAspGlyLysThrTyrAspAsnIleAlphe

95

Db

3

ATTAACTACTTGTAGCTTGAGCTAGGTGATGAAACATATGATATATGCAATT

62

Qy

96

GlUGInAlaTAGInGluIaCysSerSerArgThrProValGlnPhoValValProIys

115

Db

63

GAGCAAGCAATGAACTGAAGGAGTGTCTAGTCAGAACATATGATATATGCAATT

122

Qy

116

AsnLy/SerAsnTyrLeuAlaLysGlnIleThrPheSerGlyProCysArgSerSerIleSer

135

Db

123

AACAGAAATTAATCTCTCACCAAACTTTCAGGATCTCATTTCA

182

Qy

136

ValYsIlePheGlySerIleGluIaLysSerSerIleSerAspTLYsIleSpaGarg

155

Db

183

GTAAGATTTGTGGATCCCTAGAGCATCTAGTAATTCAGACTACAGAAGTAGAGG

242

Qy

156

LeuTrpIleAlaPheSerSerValGlnAsnLeuValValGlyGlyGlyThrIleAsn

175

Db

243

CTTGATGATCTTGTAGTGTCAAATTAGTGTGTGAGGAGGAACTATCAT

302

Qy

176

GlyAsnGlyValValTrpProSerSerCysLysIleAsnIleSerLeuProCysArg

195

Db

303

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362

Qy

196

AspAlaProThrAlaLeuThrPheTrpAsnCysLysIleAsnLeuValAsnLeuLys

215

Db

363

GATGCACCAACGCGCTAACCTCTGGATTCACAAATTGAGATGAAATCTAAAG

422

Qy

216

SerIleSerAlaGlnGlnIleAsnIleIleSerIlePheGluUserCysThrAsnValValAlaSer

235

Db

423

ASTAAATATGACAACAAATCAATCAATTGACTGACTAGTGTGACTCA

482

US-10-691-374-2 (1-457) x AW442241 (1-677)

Qy

189

AspIleSerLeuProCysArgAspAlaProThrAlaLeuThrPheTrpAsnCysLysAsn

208

Db

1

ATAAAATCAGCCGCTGAGGATGCCAACGCGCTTAACCTCTGGATTCACAAAT

60

Qy

209

LeuIleValAsnIleLysSerIleGlnGlnIleIleIleSerIlePheGluUser

228

Db

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120

Qy

229

CysteInAlaValAlaSerAsnLeuIleLeuAsnIleSerAsnSerAsnAsn

248

Db

121

TGCATCTAGTTGAGCTGCTCAATTGATGATGATGTCAGTCAGCTGAAAGAGCCAAATCT

180

Qy

249

AspGlyValIleValValAlaSerAsnSerIleSerIleSerAspThrIleLeuGlyThr

268

Db

181

GATGAGTCATGATCATACATCATATCAATATCTGATACTATTGAGAACAA

240

RESULT 10

AW442241

LOCUS

EST311637

mRNA

linear

EST

18-MAY-2001

ACCESSION

AW442241

VERSION

AW442241.1 GI:6977492 EST.

KEYWORDS

ORGANISM

Lycopersicon esculentum (tomato)

REFERENCE

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta;

Magnoliophyta, eudicots;

asterids;

lamiids;

Solanales;

Solanaceae;

Solanum;

Lycopersicon.

AUTHORS

Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and

Alcalá, J., Vrebalov, J., White, R., Bowman, C.L., Abn, S.,

Upton, J., Hansen, T., Craven, M.B., Banks, D., and

Giovannoni, J.

Generation of ESTs from tomato fruit tissue

Unpublished (1999)

Contact: CUGI

Clemson University Genomics Institute

FEATURES

source

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TM496"

/db_xref="taxon:4081"

/tissue_type="pericarp"

/dev_stage="red ripe (7-20 days post-breaker)"

/clone_lib="tomato fruit red ripe, TAMU"

/note="Vector: pBluscript SK(-); Site_1: EcoRI; Site_2:

XbaI; supplier: Giovanni; Fruit were tagged at the

breaker stage (first sign of lycopene accumulation on the

blossom end of the fruit) and harvested 7 days

post-breaker (fully red-ripe), 10 days post breaker, and

20 days post-breaker (over-ripe). 20 day fruit which

showed external or internal signs of pathogenesis were

discarded. Fruit were cut in half and the seeds and

locules were discarded prior to freezing the pericarp."

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-691-374-2 (1-457) x AW442241 (1-677)

Qy

189

AspIleSerLeuProCysArgAspAlaProThrAlaLeuThrPheTrpAsnCysLysAsn

208

Db

1

ATAAAATCAGCCGCTGAGGATGCCAACGCGCTTAACCTCTGGATTCACAAAT

60

Qy

209

LeuIleValAsnIleLysSerIleGlnGlnIleIleIleSerIlePheGluUser

228

Db

61

TTGAAGTGTAACTCTAAAGAGAAATTCATTGATGTCATTCA

120

Qy

229

CysteInAlaValAlaSerAsnLeuIleLeuAsnIleSerAsnSerAsnAsn

248

Db

121

TGCATCTAGTTGAGCTGCTCAATTGATGATGATGTCAGTCAGCTGAAAGAGCCAAATCT

180

Qy

249

AspGlyValIleValValAlaSerAsnSerIleSerIleSerAspThrIleLeuGlyThr

268

Db

181

GATGAGTCATGATCATACATCATATCAATATCTGATACTATTGAGAACAA

240

Site-2: Author: Supplier: Joyce Lincoln Institute, Research. Fruit were harvested at the breaker stage (First sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

ORIGIN
Alignment Scores: Pred. No.: 5.06e-123 Score: 1160.00 Percent Similarity: 99.11% Best Local Similarity: 99.11% Query Match: 48.54% DB: 4
US-10-691-374-2 (1-457) x BM408546 (1-675)
QY 104 SerSerArgThrProValGlnPheValValProLeuAsnLeuAsnValLeuValGln 123 Db 2 TCACTAGAACACCTGTTCAATTGGTGTCTAAACAGATTAATCTTCAGCAA 61
QY 124 IleIrrPheSerGlyProCysArgSerValSerValIleSerValIlePheGlySerLeuGlu 143 Db 62 ATCACCTTTCAAGGTCATGAAATGTTGTTGATGAGAAATCAAGGCAA 600
QY 144 AlaserSerLysValSerAspTyrosAspArgArgLeuTripleAlphaAsparVal 163 Db 122 GCACTTAGTAAATTTCAGACTACAGAAGATGAAGGCTTGATCTTGTAGTT 181
QY 164 GluAsnLeuValValIgLyGlyGlyIgLyThrIleAsnGlyAsnGlyIgLyValValIgLy 183 Db 182 CAAATTAGTTAGTTGAGGGAGGAACTCAATGCAATGGCAAGTAGTGGCC 241
QY 184 SerSerCysLysIleAsnLeuSerLeuProCysArgAspAlaProThrAlaLeuThrPhe 203 Db 242 AGTCTTGCAAAATAATACGCGCCATGCAACCGCTTAACCTTC 301
QY 204 TrpAsnCysLysAsnLeuIgLyValAsnLeuIgLySerLeuIgLyAsnLeuIgLyIleHis 223 Db 302 TGGAAATGTCGAAATTGAGAATTCATTAAGGTAAATCCACAACTCAT 361
QY 224 IleIrrPheGluSerCysSerValAspValValIleSerValIlePheGlySerLeuGlu 243 Db 362 ATCAATTGTTGTCAGCAGTAACTGTTGATGCAATTGATGCAATGCTTCAGCA 421
QY 244 LysSerProAsnThrAspGlyValIleValSerAsnThrGlyIleGlySerAsp 263 Db 422 AGAGGCCAAATACTGATGATGTCATGTCATAACTCATATACTCATGAT 481
QY 264 ThrIleIgLyThrGlyAspCysBileSerIleValSerGlySerGlnAsnValGln 283 Db 482 ACTATATGGACAGGTGATGATGATCTTCAATGTTGCTGGATCTCAAAATGCGAG 541
QY 284 AlathAsnIleIrrCysGlyProGlyIgLyIleSerIleGlySerLeuIgLy 303 Db 542 GGCACAAATTACTGIGGTCAGGTATGATGATGATGATGATGATGATGATGGA 601
QY 304 AsnSerGluIleValSerAsnValThrValAsnGluIleAsnLeuIgLyIgLy 323 Db 602 ATTCAGAACTTGTCTCAATGTTACTGTTAATGAGGCAAAATTATGGTGCAGGA 661
RESULT 12
AW221785 LOCUS AW221785 mRNA linear EST 18-MAY-2001 DEFINITION EST298996 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA ACCESSION AW221785 VERSION AW221785.1 GI:6533469
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1. . 675 /tissue_type="Pericarp" /dev_stage="breaker" /lab_host="SOLR" /clone_1b="tomato breaker fruit" /note=vector: pBluescriptSKMCUdapt; Site-1: EcoRI;

KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
AUTHORS 1. (bases 1 to 672) Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
 Roning,C.M., Fraser,C.M., Martin,G.B., Bowman,C.L., Ahn,S., and Giovannoni,J.
TITLE Generation of ESTs from tomato fruit tissue
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>

FEATURES 5 prime sequence.
source Location/Qualifiers
 1. .672
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 /mol-type="mRNA"
 /cultivar="TA96"
 /db_xref="taxon:4081"
 /clone="CLEN3L22"
 /tissue-type="pericarp"
 /dev_stage="red ripe (>-20 days post-breaker)"
 /clone_1.lib="tomato fruit red ripe, TAMU"
 /note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XbaI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
ORIGIN

Alignment Scores:
Pred. No.: 9.776-123
Score: 99.10%
Percent Similarity: 99.10%
Best Local Similarity: 48.43%
Query Match: 2
DB: 1
US-10-691-374-2 (1-457) x AW221785 (1-672)
QY 90 TyraspastilealapheduglinalatrpasnglualacysSerSerArgThrProVal 109
Db 3 TATGATAATTATGCCATGGAGCATGGATGAAGCATGTCATCTAGACACTGTT 62
QY 110 GlpheValValProLyAsnlysAsnTyreleuLeuLysGlnlethrPresarlyPro 129
Db 63 CAATTGTGGTCTCTAAACAGAATTATCTCTCAAGAACTTTCAGTCA 122
QY 130 CyargsrserserleServallysIlePheGlySerleughuaLaserSryLysIleser 149
Db 123 TCGAATCTTCTATTCAGTAGATTTGATCCCTAGAGCTCTAGAAATTCA 182
QY 150 AsptylysBspargArgLerTriplealaphesSerValGlnasnLeuValValGly 169
Db 183 GACTACAAGATAAGAGCTTGTGATTGCTTGATGATGCTCAATTAGTGTCGA 242
QY 170 GlyglylytrylIleasnGlyAsnGlyGlnValTrpTrpProSerSerCysAspIleasn 189
Db 243 GGAGGAGGAACTATCATCATGCAATGCAAGCTTACCTCTGGATGCTCAAATTG 302
QY 190 LysSerleuPcOcysArgAlaProThrAlaLeuThrPhetPAspCyslysAsnLeu 209
Db 303 AATCACTGCGCATGCAGGGAGCACACGGCTTACCTCTGGATGCTCAAATTG 362

FEATURES 5 prime sequence.
source Location/Qualifiers
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 /cultivar="TA96"
 /db_xref="taxon:4081"
 /clone="CLEN11F14"
 /tissue-type="pericarp"
 /dev-stage="red ripe (>-20 days post-breaker)"
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 /note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XbaI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
ORIGIN

Alignment Scores:
RESULT 13
AW223400
DEFINITION EST300211 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA clone CLEN11F14, mRNA sequence.
ACCESSION AW223400
VERSION AW223400.1 GI:6535084
KEYWORDS EST.
SOURCE
ORGANISM Lycopersicon esculentum (tomato)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
AUTHORS 1. (bases 1 to 643) Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Roning,C.M., Fraser,C.M., Martin,G.B., Bowman,C.L., Ahn,S., and Giovannoni,J.
TITLE Generation of ESTs from tomato fruit tissue
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>

FEATURES 5 prime sequence.
source Location/Qualifiers
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 /organism="Lycopersicon esculentum"
 /mol-type="mRNA"
 /cultivar="TA96"
 /db_xref="taxon:4081"
 /clone="CLEN11F14"
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 /note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XbaI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
ORIGIN

	COMMENT	ORGANISM	FEATURES
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.20%	Indels:	0
DB:	2	Gaps:	0
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Qy	90 TyrAsparagineAlaPheGluGlnAlaTrpArgGluAlaCysSerSerArgThrProVal	Length:	109
Db	3 TGTGATATAATGCTTGAGCAAGCTGGATGAGCTTGATGACGTCATGAGACCGTT	Matches:	213
Qy	110 GinPheValAlaProLysAsnAspAsnTyrLeuIleGlnIlePheAspGlyPro	Conservative:	0
Db	63 CATTGTTGGCTCTAAACAAAGATATTCCTCTGAGAACTTCAGGTTCA	Mismatches:	0
Qy	130 CyDArgSerSerIleSerVallysIlePheGlySerIleGluAlaSerSerIleSer	Indels:	0
Db	123 TGAGATCTTCTTATTCAGTAAGATTGGATCCCTTAGAACATGCTGAAATTCA	Length:	129
Qy	150 AspTyRAspAspArgAlaPheAspSerValGlnAlaLeuIleValGly	Matches:	182
Db	183 GACTACAAGAGAAGAGCCTTGATGCTTGATGTTGTCAAATTCTGGA	Conservative:	0
Qy	170 GlyGlyGlyThrIleAsnGlyAsnGlyGlnValTrpProSerSerCysLysIleAsn	Mismatches:	169
Db	243 GGGAGGAACTATCATGGATGGATGAGATGGCCAGTCTGCAATTCTGGA	Indels:	0
Qy	190 LysSerIleProCysAspAspIleProThrIleLeuThrPheProSerSerCysLysIleAsn	Length:	302
Db	303 AAATCACTGCATGCAGGGATGCCAACAGCCTTAACCTCTGGAAATTG	Matches:	209
Qy	210 LysValAlaValLeuIleSerIleBasaIlaGlnIleLeuIleLeuIlePheGluSerCys	Conservative:	362
Db	363 AAATGATACTAACTAAGAATTAAGCACAAATTCTCAATTCTGTC	Mismatches:	229
Qy	230 ThrAsnValValAlaSerAspIleMetLeuAlaSerAlaSerIleSerProAsnThrAsp	Indels:	422
Db	423 ACTAATGTTGATCTCATTGATGATGATGCTTCAGAGGCCAAATCTG	Gaps:	482
Qy	250 GlyValIleAlaSerAnthralinTyroIleGlnIleSerAspThrIleIleGly	Length:	269
Db	483 GGATCCATGTTGAACTACTCTATAATTCTAAATCTGATGACTATTTGACAGGT	Matches:	542
Qy	270 AspAspCysIleSerIleValSerGlySerGlnAlaValAlaIleThrCys	Conservative:	289
Db	543 GATGATGTTATTCAATTGTTCTGATCTCAAATCTGAGCCACAAATTACTGT	Mismatches:	602
Qy	290 GlyProGlyIleGlyIleSerIleGlySerIleAsn 302	Indels:	641
Db	603 GTTCCAGGTCTATGTTAGTATTGGAGCTTGGATCT 641	Gaps:	
RESULT 14			
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DEFINITION	mRNA	Matches:	216
DESCRIPTION	lineare EST 18-MAY-2001	Conservative:	0
CLONE	EST299033	Mismatches:	0
AUTHOR	tamU	Indels:	1
VERSION	1	Gaps:	0
KEYWORDS			
SOURCE			
ORGANISM	Lycopersicon esculentum (tomato)		
REFERENCE	1 (bases 1 to 672)		
AUTHORS	Alcalá,J., Vrbalov,J., White,R., Matern,A.L., Holt,I.B., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tankley,S.D. and Giovannoni,J.		
TITLE	Generation of ESTs from tomato fruit tissue		
JOURNAL	Unpublished (1999)		

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 5, 2005, 00:17:31 ; Search time 661 seconds

{without alignments} 4102.523 Million cell updates/sec

Title: US-10-691-374-2

Perfect score: 2390

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Scoring table: BLOSUM62

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Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
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Searched: #401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANSIhuman40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=LOCAL -OUTFMT_PTO -NORM=ext -HEAEST=2E500 -MINLEN=0
-MAXLEN=20000000 -USER=US10691374 @CGN_1_1_723 @runat 28022005_120708_21090
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LOGLOG -DBV TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOPA10 -YGAPEXT=0.5 -DELOP=6 -DELEXIT=7

Database : Published Applications NA: *

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11:	/cggn_6/pctodata/2/pubpna/us10_PUBCOMB.seq:*
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13:	/cggn_6/pctodata/2/pubpna/us10_PUBCOMB.seq:*
14:	/cggn_6/pctodata/2/pubpna/us10B_PUBCOMB.seq:*
15:	/cggn_6/pctodata/2/pubpna/us10C_PUBCOMB.seq:*
16:	/cggn_6/pctodata/2/pubpna/us10_I_PUBCOMB.seq:*
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18:	/cggn_6/pctodata/2/pubpna/us10_N_PUBCOMB.seq:*
19:	/cggn_6/pctodata/2/pubpna/us11_NEW_PUB.seq:*
20:	/cggn_6/pctodata/2/pubpna/us11_NEW_PUB.seq:*
21:	/cggn_6/pctodata/2/pubpna/us60_NEW_PUB.seq:*
22:	/cggn_6/pctodata/2/pubpna/us60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1820	76.2	5822	US-09-924-197-1 Sequence 1, Appli
2	1505	63.0	7456	US-10-691-374-1 Sequence 1, Appli
3	1498	62.7	7456	US-10-691-374-47 Sequence 47, Appli
4	1498	62.7	7456	US-10-691-374-49 Sequence 49, Appli
5	1127	47.2	1621	US-10-739-930-530 Sequence 530, Appli
6	1113	46.6	1631	US-10-151-668-1 Sequence 1, Appli
7	1103	46.2	1657	US-10-787-958-31 Sequence 311, Appli
8	1103	46.2	1707	US-10-739-930-1548 Sequence 1548, Appli
9	1011	42.3	1182	US-10-437-963-24607 Sequence 24607, A.
10	1010	42.3	1359	US-10-437-963-24608 Sequence 24608, A.
11	988.5	41.4	1335	US-10-437-963-28561 Sequence 28561, A
12	971.5	40.6	1168	US-10-260-238-638 Sequence 618, App
13	940	39.3	1372	US-10-425-115-33752 Sequence 33752, A
14	870	36.4	1308	US-10-425-114-30261 Sequence 30261, A
15	808	33.8	1573	US-10-437-963-2002 Sequence 52002, A
16	785	32.8	1886	US-10-425-115-82276 Sequence 82276, A
17	770	32.1	1623	US-10-425-115-82275 Sequence 73025, A
18	739	30.9	1723	US-10-437-963-73025 Sequence 70206, A
19	734	30.7	1512	US-10-437-963-70206 Sequence 70206, A
20	733.5	30.7	1822	US-10-739-930-2789 Sequence 2789, Ap
21	728	30.5	1631	US-10-425-114-9445 Sequence 9445, Ap
22	728	30.5	1984	US-10-424-559-92601 Sequence 92601, A
23	727	30.4	1673	US-10-362-091-3 Sequence 31774, A
24	726.5	30.4	2007	US-10-425-115-3138 Sequence 3138, AP
25	723.5	30.3	1479	US-10-424-559-14807 Sequence 141807, AP
26	709.5	29.7	1733	US-10-739-930-1144 Sequence 1144, AP
27	702.5	29.4	1185	US-09-938-842A-2220 Sequence 2520, AP
28	702.5	29.4	1185	US-09-938-842A-2220 Sequence 2520, AP
29	702.5	29.4	1203	US-10-425-114-32557 Sequence 52557, A
30	700	29.3	1884	US-10-425-114-3023 Sequence 3023, AP
31	700	29.3	1919	US-10-425-115-29068 Sequence 129008, A
32	699	29.2	1633	US-10-425-114-6774 Sequence 6774, A
33	691.5	28.9	1844	US-10-739-930-2788 Sequence 2788, AP
34	682	28.5	2179	US-10-437-963-22557 Sequence 56617, A
35	681	28.5	2214	US-10-437-963-98867 Sequence 59867, A
36	679.5	28.4	1374	US-10-437-963-43683 Sequence 43683, A
37	666	27.9	1182	US-10-437-963-13631 Sequence 13631, A
38	660	27.6	1599	US-10-437-963-33478 Sequence 33478, A
39	656.5	27.5	1943	US-10-425-115-10070 Sequence 10070, A
40	655	27.4	1388	US-10-425-114-2956 Sequence 4296, AP
41	655	27.4	1473	US-10-425-114-7989 Sequence 17989, A
42	654.5	27.4	1455	US-10-425-114-14146 Sequence 14146, A
43	654.5	27.4	1472	US-10-424-559-95670 Sequence 95670, A
44	654.5	27.4	1701	US-10-424-559-14782 Sequence 44782, A
45	653.5	27.3	1312	US-10-425-114-14060 Sequence 14060, A

ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/09924197
; Publication No. US0030018933A1
; GENERAL INFORMATION:
; APPLICANT: Gutierrez, Neal
; ATTORNEY: Oeller, Paul
; TITLE OF INVENTION: Improved Methods of Gene Silencing Using Inverted
; TITLE OF INVENTION: Repeat Sequences
; FILE REFERENCE: 012176-108105
; CURRENT APPLICATION NUMBER: US/09/924, 197
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/222, 508
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 3
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
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US-09-924-197-1

Alignment Scores:
Pred. No.: 4.28e-200
Score: 1820.00
Percent Similarity: 100.00%
Best Local Similarity: 99.71%
Query Match: 76.15%
DB: 10

US-10-691-374-2 (1-457) x US-09-924-197-1 (1-5822)

QY 112 ValValProLysAsnLysSerThrIleLeuLysGlnIleThrPheSerGlyProCysArg 131
Db ::::::::::::::::::::: 1387 ATGGTTCCTAAACAGAAATCTTCAGCAACTTCAGTCAGCCATGCCA 1446
QY 132 SerSerIleSerValLysIlePheGlySerLeuGluIleSerLeuGluAspGlu 451
Db 1447 TCTCTATTCAGTAAGATTGATCTTGATCTTAGAGCTAC 151
QY 152 LysAspArgArgAlaIleAspLeuAspSerValGlnAsnLeuValGlyGly 1506
Db 1507 AAAGATAGAGGGCTTGTGTTGATAATTAGTTAGTTGGAGGA 1566

QY 172 GlyThrIleAsnGlyAspGlyGlnValTrpIleProSerSerCysValIleLeuAspSer 191
Db 1567 GGAATCTATCATGGCAATGGCAAGTATGCGCAAGTCTGCAAAATAATCA 1626

QY 192 LeuProCysArgAspAlaProAlaLeuThrPheTrpAsnCysLysAsnLeuVal 211
Db 1627 CTSCCATGCGGATGCAACACGCGCTAACCTCTGAGATGCCAAATTGAGTG 1686

QY 212 AsnAsnLeuIleSerLysSerLysAsnIleAlaGlnIleHistIlePheGluSerCysThrAsn 231
Db 1687 AATAATCTAAAGCTAAATGCAACAAATCATCAATTGCAATTGACTAAAT 1746

QY 232 ValValIleSerIleSerIleAsnIleSerAlaSerAlaSerProAsnThrAspGlyVal 251
Db 1747 GTGTTAGTTCTAAATTGATGATCAATGCTTCAGCAAGAGCCAAATACTATGGAGTC 1806

QY 252 HisValSerAspThrGlyTyrIleGlnIleAspThrIleGlyThrGlyAspAsp 271
Db 1807 CAGTATCAATACATCATATCATATCATGATCATATTATGATATTGAAACGGGTGATG 1866

QY 272 CysLeSerIleValSerGlySerGlnAsnValGlnIleAsnIleThrCysGlyPro 291
Db 1867 TGTATTCAATGTTCTGGATCTCAAATGCGCCACAAATTACTGTGGTCCA 1926

QY 292 GlyHisGlyIleSerIleGlySerGlyAsnSerGluIleValSerAsn 311
Db 1927 GTCATCGCTGATTAAGTGGAGCTTGGAGCTTGAAGCTTATGTTGCTTAAT 1986

QY 312 ValThrValAlaGluIalAspIleIleGlyIleGluAspGlyValArgIleSerThr 331
Db 1987 GTCATCGCTGATTAAGTGGAGCTTGGAGCTTGAAGCTTATGTTGCTTAAT 2046

QY 332 GlnglyglySerGlyGlnIleSerAsnIleIysPheLeuAsnValGluMetGlnAspVal 351
Db 2047 CGGGGAGGATCTGGACAGCTGACAACTCAATTCGTGATGCTGGAATGCGAGCT 2106

QY 352 LysTyrProIleIleAspGlnIleGlyGlyGlnIleAspGlnIleGlyProValIleGlnIn 371
Db 2107 AGTATGCCATTATAGACGCAAACTATGTTGATGACTGAACTGACACG 2166

QY 372 PheseAlaValAlaIleLysPheAspCysSerThrsnPheProGlyGluGlyIleIleMetGlu 411
Db 2167 TTTCGCGACTTCAGTCAACTTCCAGTGGAGAAATTATGAG 2286

QY 412 AsnIleAsnIleValGlyGluSerGlyIlysProSerGluIleThrCysIysAsnValHis 431

Db 2287 AATAATAATTAGCTGGAAAGTGGAAACCATCAGAGGCTACGRCAAAATGTCAT 2346

QY 432 PheAsnAlaGluHisValThrProHisCysThrSerLeuGluIleSerGluAspGlu 451
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QY 452 AlaLeuLeuTYAsnTY 457
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RESULT 2

US-10-691-374-1

; Sequence 1, Application US/10691374
; Publication No. US20040250322A1
; GENERAL INFORMATION:
; APPLICANT: McCallum, Claire
; APPLICANT: Slade, Ann J.
; APPLICANT: Cobert, Trent
; APPLICANT: Knauf, Vic
; APPLICANT: Anawan, Inc.
; TITLE OF INVENTION: Tomatoes Having Reduced Polygalacturonase Activity Caused by Non-
FILE REFERENCE: NERB 02-276
CURRENT APPLICATION NUMBER: US/10/691,374
CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 7456
TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
NAME/KEY: CDS
LOCATION: (1479)..(1757)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (1479)..(1757)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (327)..(3491)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (3696)..(3716)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (4260)..(4467)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (4567)..(4648)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (6139)..(6255)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (5602)..(5710)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (6788)..(7045)
OTHER INFORMATION:
; LOCATION: (6788)..(7045)
US-10-691-374-1

Alignment Scores:
Pred. No.: 2.48e-163
Score: 1506.00
Length: 7456
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Qy	332	- - - - -	332
Db	5856	GTTATATGAAAAAATGTCAGAACTTCAGATATTGTA	5911
Qy	332	- - - - -	332
Db	5916	GTGTGCTTGTGAAAGTTGGTTATCCAGTTGGCTCATTTAACCAACTTA	5971
Qy	332	- - - - -	332
Db	5976	TAATGAAAGGGCTCAAACGGCCGCCACTAGTGCCTAGTCATAGGAGACTCAC	6031
Qy	333	- - - - -	332
Db	6036	GTCTGTTATTTCAGATGGACGTTCTGGTGAATGTTAATTAATTAATTAACA	6091
Qy	333	- - - - -	332
Db	6096	TGTATTAAGCATTATAAATTAATGCGTTAATATGTTAGGAGAGCTGCAC	6151
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Db	6156	TAGGCCATCAATTCTGAATGTCGAATGCAASAGTTAGTTCCUATATAGA	6216
Qy	358	PGLasnTyrCysAlaPargValGluProCysIleGln-	370
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Db	6456	GAATATCATAGAAAAATGTTAGATATATCTAAATTATTAATGAGCTT	6511
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Db	6935	AACCATCGAGGCTAAGTGCAAAATGTCATTTACAATGCTGAACTGTACCCAC
QY	441	1sCyBTh-SerIeugLileSerGluAspGluIaLteLeuLeuTyraSibYsTyr
Db	6996	ACTGCACTCACTAGAAATTCTGAGGGTGAAGCTCTTGTAAATTAT
	7045	
	6995	

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QY	192 -		QY	296 -	296
Db	3578 GGTGTCACAATGCATCACATTAGAGATTCGACCAATTAGTTATGTAATCA 3637		Db	4657 TTTCACAAATACTGTTGCAATTTCCTCATAAAGGTATGATATATAA 4716	
QY	193 -		QY	296 -	296
Db	3638 ATTTCAAGAGCATCTTGCTTGACTGTATGGTACCCCTTTCTCATGCAGCC 3697		Db	4717 TTACTTAATCCTTATTATTATGGCAATTTCCTGCTTATGGTAAAT 4776	
QY	193 OCYB ATGABP Alaprothr--		QY	296 -	296
Db	3698 ATGCAGGGATSCACCAACGGTACGTAAITGATTGATTAAGAAAAAGCTA 3757		Db	4777 GACTTAGACACAATAATTAGGCCGTUTGGATGGCATAAAAGCAGCTTAAAGTA 4836	
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Db	3878 AATTAGATATCAAAACTATTGAAATTACTATAATTGCAATTTCATATCA 3937		QY	296 -	296
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QY	199 -		Db	5137 AGCTTTAAGTCAGTTGACCAGCTTTAAGCTGAGCTAAAGAGCTTAAATGCTG 5196	
Db	3998 ACAACACATAGTAGACGGAGAAAGTATAAACATAACTCTCAAGTAGATCGATTG 4057		QY	296 -	296
QY	199 -		Db	5077 TTAAAACTTAAATAAGTGTGTTGAGTATGCCAAAGAGCTAAATGCAAAACC 5136	
Db	4058 ACACACACCTCAAACCTACCGTTCTCGATTATTCCTTAACTTCATTAAGTAA 4117		QY	296 -	296
QY	199 -		Db	5197 CTAGATGTTGCTATATATTGAGCTTTTGAGTAGTATATTCCTTAAGTCAA 5256	
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QY	199 -		Db	5257 CATAAAATACATGCTTAACTAGCACATACTGTTATCAAAGACCAAATGATGATAA 5316	
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QY	200 -	-AlaLysThrPheTrpAsnCysLysAsnLeuValAsn 212	Db	5317 TTTGCCATTGATTTCACAGAAAGGGATAGTCAAAGTGTACATTCATGATAA 5376	
Db	4238 ACTAAATGTTAAATTTCAGGCCCTAACCTCTGAAATGCAAAATTGAAAGTAA 4297		QY	296 -	296
QY	212 AsnLeuLysSerLysAsnIleGlnGlnIleHistIleLysTheGluSerCysThrAsnva 232		Db	5377 TGAAGATATCATAAAGCTAAATTAGAGAATCAATAATTGAGGATCAAATGTT 5436	
Db	4298 TATCTAAAGATTAATGACAACTTATCAATTGATGCTATGATGCTATG 4357		QY	296 -	296
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Db	4358 TCTAGCTTCATTTGATGATGATCATGCTTCGCGAAAGCCAAATCTGAGTC 4417		QY	296 -	296
QY	252 ValSerAsnThrGlyIleGlnIleSerAspThrIleIleGlyThr--		Db	5497 ATCTAAATAAACATGCAATAATTGAGCAATGTTGGTACTTAAATCTCT 5556	
Db	4418 TGTATCAATGCTCAATAATGCAAAATGATCATTATTGGAAAGCTTAT 4477		QY	297 -	1IleGlySerLeuG1 301
QY	268 -		Db	5557 GAATATTGCTCTATTTCCTTTATTTCATGGATTACTATGAGCTTGG 5616	
Db	4478 TTAAATTATTATTCGAAATTAAATTGAGGATATTATTGATAACTA 4537		QY	301 YSerGlyAsnSerGluLalaValSerAsnValThrValAsnGluLalaValileG1 321	
QY	269 -	-GlyAspAspCysIleSerIleValSerIleValSerIleValSerIleValSerIle 279	Db	5617 ATCTGGAAATCAGACGCTTGTGCTTGTGCTTACTGAAATGACCAAAATTGG 5676	
Db	4538 ATTATTAATTTTAAATTTTTATAGGTCATGATGTTATTCATGGTTC 4597		QY	321 YAlaGluAspIlyValArgIleYsrHrpTgln----- 322	
QY	279 rclnAsnValGinalaThrAsnIleThrCysGlyProGlyHisGlyIleSer-----				

Db 5677 TGCCGAATGGACTTAGGATCAAGACTGGCA-GGTACCCCCCCCCCCCC 5735 Qy 332 ----- 332

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Db 5796 ATTGATTTCATGTTGAATTATATTTGATAAGTAGTATTACTAGCTTCTAT 5855 Qy 332 ----- 332

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Db 6516 ATCTAATATTGTAGTAACTGAGAACATACATACATGACTACACAAAGGAATACAGCGATT 6535 Qy 370 ----- 370

Db 6636 CTCAACACATATAGTAACTGCAATCAATGACTACACAAAGGAATACAGCGATT 6695 Qy 370 ----- 370

Db 6696 AGAGAGGCAATTGGAAATAGAACATACATACATGAGAACATACATGAGAACATACAGCGATT 6755 Qy 371 ----- 370

Db 6756 TCTCTCAGATATTAACTGCTATTGCAAAACGAATCAATAGTAGAGTATCCCTAA 6695 Qy 370 ----- 370

Qy 381 alTyrGluasnIleLysGlyThrSerAlaThrValAlaLeuLysPheAspCysSerT 401 ; Sequence 49, Application US/10691374 ; Publication No. US20040250322A1 ; GENERAL INFORMATION: ; APPLICANT: McCallum, Claire ; APPLICANT: Slade, Ann J. ; APPLICANT: Colbert, Trent ; APPLICANT: Krauf, Vic ; APPLICANT: Anawih, Inc. ; TITLE OF INVENTION: Tomatoes Having Reduced Polygalacturonase Activity Caused by Non-FILE REFERENCE: NBRB 02-276 CURRENT APPLICATION NUMBER: US/10/691,374 CURRENT FILING DATE: 2003-10-22 NUMBER OF SEQ ID NOS: 50 SOFTWARE: Patentin version 3.1 SEQ ID NO: 49 LENGTH: 7456 TYPE: DNA ORGANISM: Lycopersicon esculentum FEATURE: NAME/KEY: CDS LOCATION: (2416)..(2547) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (1479)..(1757) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (3327)..(3491) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (3696)..(3716) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (4567)..(4648) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (4260)..(4467) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (5602)..(5710) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (6139)..(6255) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (6788)..(7045)

Db	3458	GTTGCCAATCTCTGCAAAATAATAACACTGGTATTAACTTGCTTATAAGT	3517	QY	192	-	Db	4538	AATTATAATTAAUTTTTATAGTGATGATGTATTCAATTGTTCTGCATC	4597	QY	279	RGLIANSValGlnAlaThrAsnIleLysIleCysGlyProGlyIleGlyIleSer	296
Db	3518	TTCAGCTTATGTTGCTCAATCTTAACTTGCTTAAGATATTATATGAGGA	3577	QY	192	-	Db	4598	TCAAATGCGGCCGAAATTACTTGCCAGGATGTTAG-GTACTCA	4656	QY	296	-	296
Db	3578	GGTGTCAACATGCACTCACATTAGAGATCCGACCAATTAGTTATGATCA	3637	QY	193	-	Db	4657	TTTACAAATAACTCTTCAATTCTTATTGATAAAGTAGTAGTATAATAA	4716	QY	296	-	296
Db	3638	ATTCAGAGCATCTTGCTGTACTGTGATCATGGTACCCCTTTCTCATGCAGCC	3697	QY	193	OcySarCaspAlaProThr	Db	4717	TTACTTAAACCTTAAATTATGCAATTTCCTCTGTCTTATGTTAAT	4776	QY	296	-	296
Db	3698	ATGCAAGGATGSCACCACAGGTAGTGTAAATGCAATTGATGATGATGAACTTA	3757	QY	199	-	Db	4777	GAATTCACACATAATTAGGCCCGTTGGATGGCGATAAACGAGCTTAAGCTA	4836	QY	296	-	296
Db	3758	AAATATATTGAAATTAAATGAAAGGTAAATAACTTAACTTGCCAGGACCTAT	3817	QY	199	-	Db	4837	CTTTAAAGTGTGAACATTATTAAATAAGCAGTTACCGTTGATAAAAGTC	4896	QY	296	-	296
Db	3818	TACCCCTGACTTAAATAGTGTATTAAAGATAAAAGTGTATTGAAACAA	3877	QY	199	-	Db	4897	TGAAGTTGTTATGTCACACTGAAAGGAAATGGAGAAAGAAATGTGTTAGGTTA	4956	QY	296	-	296
Db	3878	AATTAGATATTCAAAACATTGAAATTACTATAATGCAATTTCATCA	3937	QY	199	-	Db	4957	TGGTGTATTGATAAATTAAGCACAAMAGATAAAATGTGTCACTTAACCA	5016	QY	296	-	296
Db	3938	ATATGATAAATAATTAGTAAGTCTATGATTGATCTAAATAATCATG	3997	QY	199	-	Db	5017	ACTTAAAGCTACCTACCCAGCTTAACTTTGCTTAATAAGTTTT	5076	QY	296	-	296
Db	3998	ACAAACAAATAGTAGAGCGAGAACTATAACAATACCTCTCAAGTAGATGATGT	4057	QY	199	-	Db	5077	TTTAACACTAAATAAGTGTGTTGAGTATGCCAAAGAGCTTAATAATGCCAAAAACC	5136	QY	296	-	296
Db	4058	ACACACACCTCAAAACCTACAGTTCTCGATTATATTCTTATCTTAAATGAA	4117	QY	199	-	Db	5137	AGCTTTAGTCAGTTACCAAGCTTTAAGTGAGCTGAGCCAAACAGGTCTTAAATGCTG	5196	QY	296	-	296
Db	4118	TCAAAGGCTTATTAGTCCTAAATCTATCATTTGAAACTCTATCTTACGCCCTGT	4177	QY	199	-	Db	5197	CTTAGATGCTATATATTGAGCTTTGAGTAGTATATTCTTAAGTCAA	5256	QY	296	-	296
Db	4178	ACATTGAGATCTGAAACATGATGATGATATTAACTTGTTATTAAATAA	4237	QY	200	-	Db	5257	CATAAAACACATGCTTACAGACATAGTAACTAAAGAGGAATGATGATAA	5316	QY	296	-	296
Db	4238	ACTAATATGTTAACTTCAGGCCTTACCTCTCGGAATTGCAAATTGAAAGTGA	4297	QY	212	DnsLeuIysSerLysSerLysAsnIleLysSerLysAsnIleLysValas	Db	5317	TTTGCAGATTGATTCACAGAAAGGGATAGTCAGTCAGTGTACATTCAATGAA	5376	QY	296	-	296
Db	4298	TTCTTAACTGAGTAAATGCAACAACTCATCAATTGAAATTGCACTGAA	4357	QY	232	IvalAlaSerAlaLeuMetIleAsnAlaSerAlaLeuSerProAlnThrAspGlyVal	Db	5437	TACCTATTAAATACTATTCATTTCAATTAAATTACTAACTTAAAGAGTGTATA	5496	QY	296	-	296
Db	4358	TGAGCTCAATTGATGTCAGCAAGAGCCAAACTCTGAGTC	4417	QY	268	IleGlySerIleGlySerIleGlySerIleGlySerIleGlySerIleGlySerIleGly	Db	5557	GAATTTGCTCTATTTCCTTTCCTCAGGATACTATTGGAAGCTT	5616	QY	296	-	296
Db	4418	AGTATCAAACTCTCAATATCAATATCTGATCAATTGTTAGGTTATTAT	4477	QY	268	4418 AGTATCAAACTCTCAATATCAATATCTGATCAATTGTTAGGTTATTAT	Db	5497	ATCTAAACATGCAATTATGAGCAATTGTTGCTTGTACCTATAACTCT	5556	QY	297	-	296
Db	4478	TTATTTTATTCAATTAAATTAGAALAAAAGGAGTATTGATAACTA	4537	QY	269	4478 TTATTTTATTCAATTAAATTAGAALAAAAGGAGTATTGATAACTA	Db	5557	GAATTTGCTCTATTTCCTTTCCTCAGGATACTATTGGAAGCTT	5616	QY	296	-	296
Db	5617	ATCGAAATTCAAGCTTATGICIAATGTTACTGAAATGAGCCAAATTATCGG	5676	QY	279	5617 ATCGAAATTCAAGCTTATGICIAATGTTACTGAAATGAGCCAAATTATCGG	5676	QY	296	-	296			

QY 116 AsnLysAsnTyrLeuLeuLeuLysGlnIleThrPheSerGlyProCysGlySerSerLeSer 135 ; GENERAL INFORMATION:
Db 421 GGAAGACTTATCTCTTAACTGCTACTCCATTAGGCGCCGCAATCTACGTAAAC 480 ; APPLICANT: ULVSKOV, Peter
QY 136 ValValIlePheGlySerIleGluAlaSerSerSerIleSerAspIleSerAspArg 155 ; APPLICANT: CHIND, Robin
Db 481 TTTCAGATCTTAGGCACCTTATCGATCATCGAACCTTGAGTACAGAACAAAC 540 ; APPLICANT: VAN ONCKELIN, Henri
QY 156 LeuTrpIleAlaPheAspSerValGlnAsnLeuValValGlyGlyGly-...-GlyThr 173 ; APPLICANT: PRINSEN, Els
Db 541 CATGGCTTAATCTAGAGCTAACATCTACATCGAGGTGCTCACAGGAAATT 600 ; APPLICANT: BORKHORST, Bernard
QY 174 IleasnGlyAsnGlyGlnValTrpProSerSerCysValIleSerLeuPro 193 ; APPLICANT: SANDER, Lilli
Db 601 ATTAAATGGCAACGCGAAACCTGTGGCAGAATCTACGAAATCACAACTAGCA 660 ; APPLICANT: PETERSEN, Morten
QY 194 CysGargAspAlaProThrAlaLeuThrPheTrpAsnCysLysAsnLeuValAsn 213 ; APPLICANT: BOTTERMAN, Johan
Db 661 TGCACAAAGCTCAACGGCTCTACTTATACTTACAATTAGAAATTGAGTTGA 720 ; TITLE OF INVENTION: Seed Shattering
QY 214 LeuIysSerLysAsnIleGlnIleHisIleLeuPheGluSerCysThrAsnVal 233 ; FILE REFERENCE: 2121-0138P
Db 721 CTGAGGTGAAATGCCAGAGATCAGATGAAATTGAGAAATGCAAGTGTAA 780 ; CURRENT APPLICATION NUMBER: US/10/151, 668
QY 234 AlaSerAsnLeuMetIleAsnAlaSerAlaSerSerProLanThrAspGlyValHisVal 253 ; PRIORITY FILING DATE: 2002-05-21
Db 781 GTTAGTAAATGTGAGATCATCTCTCGGGATAGTCACACAGATGGTATCATTC 840 ; PRIORITY APPLICATION NUMBER: US/09/051, 239
QY 254 SerAspThrGlnIleTyroleglnIleSerAspThrIleLeuGlyTyrGlyAspPCysIle 273 ; PRIORITY FILING DATE: 1998-09-28
Db 841 ACTAAATRACTAAACATTCAGTCAGTCAGTCACATCGATATGGAAAGGGTAA 900 ; PRIORITY APPLICATION NUMBER: PCT/EP96/04313
QY 274 SerIleValIleGlySerGlnAsnValGlnIleThrAsnIleThrCysGlyProGlyHis 293 ; PRIORITY FILING DATE: 1995-10-06
Db 901 TCCATTTGAGATGGAAAGCAGAAATTTCAATCTGTAACTTGAACTTGCGGGCCGGTAC 960 ; PRIORITY APPLICATION NUMBER: EP 95 203328.0
QY 294 GlyLeuSerIleGlySerIleGlyAsnSerGluAlaIleValSerIleVal 313 ; NUMBER OF SEQ ID NOS: 14
Db 961 GGGATCAGCAATGGAGCTGGGGGAGCAATTGCGAAAGCTATGTCGGAAATTAT 1020 ; SOFTWARE: PatentIn Ver. 2.1
QY 314 ValLeuGluIleAlaIleIleGlyIleAlaGluAsnGlyValIleLeuIleThrIleGly 333 ; SEQ ID NO: 1
Db 1021 GTGGATGGCTCTAAGTCCTGAGTGACATGGAGITAGGATTAGACTATCGGA 1080 ; LENGTH: 1631
QY 334 GlySerGlyGlnAlaSerAsnIleIleGlyPhelLeuLeuValGlnAspValIleIle 353 ; TYPE: DNA
Db 1081 GGATCAGGAACTCCAGAACATTAATTCATGAAACTGGAAACGTCAGAAAT 1140 ; ORGANISM: Brassica napus
QY 354 ProIleLeuSpnGlnAsnTyrCysAspGlyGluProCysIleGlnIleSer 373 ; FEATURE:
Db 1141 CGGATCATTATCCACCAAGCACTTGCAGCAAG--GACAATGGCAAGCAGAGTCG 1197 ; OTHER INFORMATION: Location 95-163 = region encoding the presumed
QY 374 AlalValGlnIleAlaIleIleGlyIleAlaGluAsnGlyValIleLeuIleThrIleGly 393 ; OTHER INFORMATION: complementary to oligonucleotide PG5
Db 1198 GCGTGTGAAAGTCAAGCTGTTGAGATCAGAACATCTGGTACAGGCGTACGGTC 257 ; OTHER INFORMATION: Location 821-837 = region of endo-PG cDNA
QY 394 AsnIleValIleGlySerThrAsnPheProCysGluGlyIleLeuIlePheAsn 413 ; OTHER INFORMATION: corresponding to oligonucleotide PG1.
Db 1258 GCGATTAAGTGTGAAATGGCAGGAGATTCATCTCAAGGATGTTGCTGTTGAGTCG 1317 ; NAME/KEY: unsure
QY 414 AsnLeuValIleGlySerGluAlaIleCysLysAsnValHisPheAsn 433 ; LOCATION: (1439)
Db 1318 AAATAAAGCA-----GAAACAGCTCTGCAAATGCCATGTAA 1362 ; OTHER INFORMATION: Location 1059-1073 = region of the endo-PG cDNA
QY 434 AsnAlaGluIleIleValThrProHisCysThr 443 ; OTHER INFORMATION: Location 1059-1073 = region of the endo-PG cDNA
Db 1363 ATCAGGCGCCGTTCTCTAACTCT 1392 ; OTHER INFORMATION: complementary to oligonucleotide PG2

US-10-151-668-1

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	1.23e-118	1631	223	69	121	34	8
	1113.00						
	65.32%						
	49.89%						
	46.57%						
DB:							
	13						

US-10-691-374-2 (1-457) x US-10-151-668-1 (1-1631)

QY 7 SerIleLeuLeuLeuIleIlePheAlaSerSerLeSerThrCysArgSerAsnVal 26 ; GENERAL INFORMATION:
Db 119 GCTGTGTTCTCTATCGCTCTTGTGCTGCGCTGCTGCCAACCTTGAGTACAGCTA 178 ; APPLICANT: ULVSKOV, Peter
QY 27 IleAspAsnLeuPheIleGlyGlnValThrAspAsnIleLeuIleGluGlyIleAlaIle 46 ; APPLICANT: CHIND, Robin
Db 179 ---GATGAGGA-----TATGGTCA-----TATGGTCA-----TATGGTCA 196 ; APPLICANT: VAN ONCKELIN, Henri
QY 47 AspPheGlnAlaIleIlePheLeuSerIleGlySerAsnAsnIleAsp 66 ; APPLICANT: PRINSEN, Els
Db 197 GAAGATGGA-----AGCTCGAATCCGATAGTTATCAAGCTCAACAGGACG 247 ; APPLICANT: BORKHORST, Bernard
QY 67 LysVal-----AspIleAsnGlyIleIleValLeuIleAsnVal 78 ; APPLICANT: SANDER, Lilli

QY 436 GlutathioneS-transferase 442
 79 LeuSerPheGlyValAlaGlyAlaGlyAspGlyLysThrTyrAspAsnLeuAlaPheGluGlnAla 98
 :::::::::::::::::::::|||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db TCGAACCTCTGGAAACCAAGAGATGAAACACCGATGATACTCAGGCTTCAGAAGAAC 367
 99 TrpAsnGluAlaCysSerSerArgThrProValGlnPheValValProLysAlaValGluGlnAla 118
 ::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db TCGAAGGAGGCTGTCAACAATGGACTTACTACTCTTAATTCTTAAGGAAGAAAGCT 427
 119 TyrLeuLeuLysGlnIleThrPheSerGlyProCysArgSerSerLysSerValLeuSer 138
 ::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db TAATCTCTTAAGCTTATAGCTTAGATCAGAGGCCCATGCAAACTTTACGTAGCTCCAGTC 487
 428 IleAlaLeuAspSerValGlnAlaLeuValValGlyGlyGly----GlyThrIleAsn 175
 ::|||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy ::|||:|||||:|||||:|||||:|||||:|||||:|||||:
 139 PheGlySerLeuGluAlaSerSerLysIleSerAspTyr--LysAspArgArgLeuIle 157
 ::|||||:|||||:|||||:|||||:|||||:|||||:
 Db CTTAGGCACTTTATCAGCTCTCACAAACGATCGGATACAGTATGACAGAACCTGG 547
 488 ValGlyGlyGlnValValTrpProSerSerCysLysIleAsnLysSerLeuProCysArg 195
 ::|||||:|||||:|||||:|||||:|||||:
 Qy ::|||||:|||||:|||||:|||||:
 608 GSGAACGGAATAATCTGGCAAACTCATGAAATGCAATCTVAGCCATGCA 667
 ::|||||:
 196 AspAlaProThrAlaLeuThrPheTrpCysAlaLeuLysValAlaAlaLeuLys 215
 ::|||||:
 Db AAAGGCCAACGCGTCTTACTCTTACACTAAAGAATTGATGAGAATCTGAGA 727
 668 ::|||||:
 216 SerLysAlaAlaGlnGlnGlnLeuIleHisIleLysPheGluSerCysThrAlaValAlaLeuLys 235
 ::|||||:
 Qy ::|||||:
 728 CTGAGAAATGCAAGCAGTCAGATTCTGATGAGAAATGCAACAAATTGCGCTTAAG 787
 ::|||||:
 Db ACTAAACATTCGATCCTCAATTCAGATCAGATGCTGAGCTGAA 907
 848 ::|||||:
 276 ValSerGlySerGlnAlaValGlnAlaIleAsnIleThrCysGlyProCysGlyValHisValSerAla 295
 ::|||||:
 Qy ::|||||:
 236 AspLeuMetIleAlaAsnSerAlaSerAlaSerProAsnThrAspGlyValHisValSerAla 255
 ::|||||:
 Db AATGTTAAGATCCTGCTCTGGCATGTCGCCACAGGATGTTACATCGTGCCT 847
 788 ::|||||:
 :
 256 ThrglnTyrlleGlnIleSerAspThrIleIleGlyThrglnAlaSpaSerCysIleSerIle 275
 ::|||||:
 Qy ::|||||:
 848 ::|||||:
 277 ValSerGlySerGlnAlaValGlnAlaIleAsnIleThrCysGlyProCysGlyValHisValSerAla 295
 ::|||||:
 Db AATGTTAAGATCCTGCTCTGGCATGTCGCCACAGGATGTCGCCACAGGATGTTACATCGTGCCT 967.
 908 GAGGATGGGATCGCAAAATGTCATCATGATGTTACTGCGCCCTGGTCTGGATC 967.
 296 SerIleGlySerIleGlySerGlyAsnSerGlnAlaIleAsnValThrValAlaAsn 315
 ::|||||:
 Qy ::|||||:
 968 AGCATTTGGAGCTGGGATGACATCCAAAGCTTGTGAGATGTTACATCGTGCCTGGATC 1027
 968 AGCATTTGGAGCTGGGATGACATCCAAAGCTTGTGAGATGTTACATCGTGCCTGGATC 1027
 :
 316 GluAlaLysIleIleGlyValAlaGluAlaGlyValArgIleLysThrPheGlnGlyGlnSer 335
 ::|||||:
 Db GGTGCTAGCTCTGAGACTGACATGGAGTAGAACTGAGCTTACCGGAGGGCA 1087.
 1028 GGTGCTAGCTCTGAGACTGACATGGAGTAGAACTGAGCTTACCGGAGGGCA 1087.
 :
 Qy ::|||||:
 336 GlyAlaAlaSerAsnIleIleIlePheLeuAlaValGluAlaAspGlnAlaPheValIleAsnVal 355
 ::|||||:
 Db GGTGCTAGCTCTGAGACTGACATGGAGTAGAACTGAGCTTACCGGAGGGCA 1147
 1088 GGTGCTAGCTCTGAGACTGACATGGAGTAGAACTGAGCTTACCGGAGGGCA 1147
 :
 Qy ::|||||:
 356 IleIleAlaProGlnAlaIleIleIlePheLeuAlaValGluAlaAspGlnAlaPheValIleAsnVal 375
 ::|||||:
 Db ATATATGACCAAGCTACTGGCAAG 1148
 1148 ATATATGACCAAGCTACTGGCAAG 1148
 :
 Qy ::|||||:
 376 GluValAlaValValValTyrglAlaAlaIleLysGlyThrSerAlaIleValAlaLeu 395
 ::|||||:
 Db CAAGTGAACATGTCGTCGATCACAGACATAAAGGTAGAGGCCACAGATGTCGGATA 1264
 1205 CAAGTGAACATGTCGTCGATCACAGACATAAAGGTAGAGGCCACAGATGTCGGATA 1264
 :
 Qy ::|||||:
 396 LysPheLeuAspCysSerThrAsnAlaProCysGluGlyIleLeuMetGluAsnIleAsnLeu 415
 ::|||||:
 Db ATGTTAATGCACTGCTGAATTCATCCAGGTGATGCTGAGATGTCACATC 1324
 1265 ATGTTAATGCACTGCTGAATTCATCCAGGTGATGCTGAGATGTCACATC 1324
 :
 Qy ::|||||:
 416 ValGlyGlySerGlyLysProSerGluAlaIleAsnAlaIleAsnAlaIleAsnAla 435
 ::|||||:
 Db 1325 AAAGCA-----GGAAAGCTCTGGCAAAATGCTCACTTAAGCTAA 1369
 :
 Qy ::|||||:
 161 AspSerValGlnAlaLeuValValGlyGlyGly----GlyThrIleAlaGlyAla 178
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 :
 US-10-787-958-31 RESULT 7
 ; Sequence 31, Application US/10787958
 ; Publication No. US2004015405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watt, Paul
 ; APPLICANT: Robert, Jeremy A.
 ; APPLICANT: Whitelaw, Catherine
 ; TITLE OF INVENTION: Signal Transduction Protein Involved in Plant Disease
 ; FILE REFERENCE: 0623.830000
 ; CURRENT APPLICATION NUMBER: US/10/787, 958
 ; CURRENT FILING DATE: 2004-03-27
 ; PRIOR APPLICATION NUMBER: GB806113.8
 ; PRIOR FILING DATE: 1998-03-20
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 31
 ; LENGTH: 1657
 ; TYPE: DNA
 ; ORGANISM: Brassica napus
 ; FEATURE: CDS
 ; NAME/KEY: CDS
 ; LOCATION: (145)..(1443)
 ;
 US-10-787-958-31 Alignment Scores:
 ;
 Prod. No.: 1.85e-117 Length: 1657
 Score: 1103.00 Matches: 221
 Percent Similarity: 65.54% Conservative: 70
 Best Local Similarity: 49.77% Mismatches: 125
 Query Match: 46.15% Indels: 28
 DB: 18 Gaps: 7
 US-10-691-374-2 (1-457) x US-10-787-958-31 (1-1657)
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 Qy 7 SerIleLeuAlaIleLeuIleIlePheAlaSerSerLysSerThrCysArgSerAlaVal 26
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 Db 169 GCTATTTCTTATCGCTGCTTCTTGATGCTGCTGCAAGCTTGAGCTGACAGTA 228
 :
 Qy 27 IleAsp----AspAsnLeuPheLysGlnValTyRAspAsnIleLeuGlu 41
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 Db 229 GATGATGGATATGGTCATGAAAGTGGAAAGCTTCGAAACC----GATAGTTAATCAAG 282
 :
 Qy 42 GluGluPheAlaHisAspPheGlnAlaIleAsnSerTyRLeuSerTyRLeuSerLysAlaIleGluSer 61
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 Db 283 CTCACACAGGAGCACCTTCTACCTGAAAGCTCGGATAGACCACCTACCGAATCA 342
 :
 Qy 62 AspAsnAsnIleAspLysValAspLysAsnGlyIleLysValIleAsnValLeuSerPhe 81
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 Db 343 TCA-----ACTGTAGTGTCTGACTC 366
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 Qy 82 GluAlaLysGlyAspGlyLysThrTyrAspAsnLeAlaPheGluGlnAlaTrpAlaGlu 101
 ::|||||:
 Db 367 GAGCAAAAGGTGTGAAACACGGATGATCTAGGCTTCAGAAGCATGGAGAG 426
 :
 Qy 102 AlaCysSerSerArgThrProValGlnPheValValProLysAlaValTyRLeu 121
 ::|||||:
 Db 427 GATGTCAACAAATGGAGTGCACATCTCTGATTCAGGAGACTACTCTCT 486
 :
 Qy 122 LysGlnIleThrPheSerGlyProCysArgSerSerLysSerValLeuSerPhe 141
 ::|||||:
 Db 487 AGCTTATGAGTCAGAGGCCATGCAAACTTACATGAGCTCCAGTCCTGGACT 546
 :
 Qy 142 LeuGluAlaSerSerLysIleSerAspTyr--LysAspArgArgLeuIleAlaPhe 160
 ::|||||:
 Db 547 TATCAGCTCTTACAAACGATTCGGATTACAGTATGACAGAACCACTGGCTTATGG 606
 :
 Qy 161 AspSerValGlnAlaLeuValValGlyGlyGly----GlyThrIleAlaGlyAla 178
 ::|||||:
 :

607 GAGGAGCGTTAAATCTCATCGTGCCTCGCCGGGATTGTCATGCCAACGGA 666
 QY ; TYPE: DNA
 179 GlnValTryptProSerSerCysLysIleAsnLysSerLeuProCysBargPalaPro 198
 Db ; ORGANISM: Brassica napus
 QY ; FEATURE:
 OTHER INFORMATION: Clone ID: BRANA-23APRO3-CLUSTERS3_1
 US-10-739-930-1548
 Alignment Scores:
 Pred. No.: 1.95e-117 Length: 1707
 Score: 1103.00 Matches: 221
 Percent Similarity: 65.54% Conservative: 70
 Best Local Similarity: 49.77% Mismatches: 125
 Query Match: 46.15% Indels: 28
 DB: Gaps: 7
 727 AACCTGCTACTCTACACTAACCTAACATTGATGAGAATGAGATGAGAT 726
 199 ThralAlleLurhrPherTrpAsnCysLysAsnLeuLysValAsnLeuLysSerLysAsn 218
 219 AlagInglleHsIleLysPheGluSerCysThrAlnValValAlaSerAsnLeuMet 238
 786 787 GCACAGCACATTCAAGATTCAGATTCAGATTCAGATGAGAATGCAACAGTGAGAT 846
 239 IleasnAlaSerAlaLysSerProAsnThrAspGlyValHisValSerAsnThrGlnTyr 258
 847 ATCAGCTGCTCGCTCGATGTCCTCAAACGGGATGGTTTCAATCGTGTCAAAAC 906
 259 IleGlnIleSerAspThrIleLysIleGlyThrGlyAspAspCysIleSerIleValSerGly 278
 907 ATTGAAATCTCCATTAGACATGACATGGCAAGGTGATGATGATGATGATGATGATGGA 1026
 966 279 SerLeuGlySerGlyAsnSerGluAlaTyValSerAsnValAlaValAlaGluAlaLys 318
 1027 AGCTGGGGGATGACATTCAAAGTTATGTTATGGAATTGTTGAGCTTACCG 1086
 319 IleIleGlyIlaGluGlyValAspGlyLysIleThrCysGlyProGlyHisIleSerIleGly 298
 967 TCGCAAAATGTCAAATCAATGATGATGATGATGCGCCCGGTCATGCATCAGCTTGA 1026
 299 SerLeuGlySerGlyAsnSerGluAlaTyValSerAsnValAlaValAlaGluAlaLys 318
 1027 AGCTGGGGGATGACATTCAAAGTTATGTTATGGAATTGTTGAGCTTACCG 1086
 340 341 SerLeuGlyIlaGluGlyValAspGlyLysIleThrCysGlyProGlyHisIleSerIleGly 298
 968 TCGCAAAATGTCAAATCAATGATGATGATGCGCCCGGTCATGCATCAGCTTGA 1026
 1087 CTCCTCTCAGACTGACATGAGGAGTAAGATCAGACTTACCGGTCAGGACTGCT 1146
 359 GlnAsnTyrCysAspArgValGluProCysIleGlyGlnGlyPheSerAlaValGlnVal 1206
 339 SerAsnIleLysPheLeuAsnValGluMetGlnAspValPheLysTyrProIleIlePhe 358
 1147 AACGACATTAATCCAAACATTCGTTATGATGATGTCAGATTCGATCATTCGAC 1206
 359 GlnAsnTyrCysAspArgValGluProCysIleGlyGlnGlyPheSerAlaValGlnVal 1206
 1207 CAGACTCTGCGCAAGA---GAAATGCGACAAAGCAAGAACTGCGCTCAGTGAC 1263
 379 AsnValValTyrGluAsnIleLysGlyIleGlyIleSerAlaAlrLysValAlaIleLysPheAsp 398
 1264 AACGCGTGATTCGAACTACAAAGTACAGGAGCCACAGGATGCTGCGATAATGTTAT 1323
 399 CysSerThrAsnpheProCysGlyGluIleIleMetGluAsnIleAsnLeuValGlyGlu 418
 1324 TGCAGTGAAATATCCATGCCAGGTTGCTGCTGAACTCAAGGA--- 1380
 419 SerGlyLysProSerGluAlaLurhrPherTrpAsnValHisPheAsnAsnAlaGluHisVal 438
 1381 -----GGAAGCTCTGCAAAATGTCAGTTAGGTTAAGGGCACCGT 1428
 439 Thr-Pro-His-Cys 442
 1429 TCTCTTAAATGTC 1440
 ,-----SULT 8-----
 Sequence 1548, Application US/10739930
 Publication No. US20040216190A1
 GENERAL INFORMATION:
 APPLICANT: Kovacic, David K.
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
 FILE REFERENCE: 38-21(53377)B
 CURRENT APPLICATION NUMBER: US/10739, 930
 CURRENT FILING DATE: 2003-12-18
 NUMBER OF SEQ ID NOS: 11088
 SEQ ID NO: 1548
 LENGTH: 1707

Qy 967 TCGCAAAATGTCATCATGATTAACTTGCCCCGGTCAGGCATCAGGATTCAGCTGCA 1026
Db 79 GGCAGTAATGTTCAGCTACAGACTGGGCCATGGAGCGGACATGATGAC 138
Qy 92 AsnIleAlphegluglalatpAspGluIleSerArgLysProValInPhe 111
Db 139 ACCAAGCATTGGAGATACTAGCTGAGCTGCTCTCTGCAAACCTGGAGTTG 198
Qy 319 IleIleGlyIlaGluIaGlyIvaLgIleYsthrTrpGlyGlySargYGlnala 338
Db 1087 CTCCTGAGACTGACAACTCCAAAGCTTGTGTTGAACTGGGAATTATGCTGCTGGCT 1086
Qy 339 SerAsnIleIleSpheLeuAsnValGluMetGlnAspValIstyrProIleLeP 358
Db 1147 AAGACATTAATCCAAACATCGTATGATGAGTAACTGAGATTCAGGGTCATATCGAC 1206
Qy 359 GlbntTyCybasPargValgIluProCysIleGlnIpheSerAlaValGinValys 378
Db 1207 CAGACTACTGCGAACAG---GACAATCGAACACAGAACTGCGATTCAGTGAC 1263
Qy 379 AsnValValTyrgluAsnIleIleValGlyThrSerIlaThrLysValAlaIleIlePheAsp 398
Db 1264 AATGTCGCTATCGAACATCACAGGTAGAGGCCACCGATGCGCTAATGTTTAT 1323
Qy 399 CySSerThrAsnpheproCysIgIgluYIleIleMetGluAsnIleAsnIleAsnIleValGlyGlu 418
Db 1324 TGCGTGAAATTCATCCAACTGATGTTGAGATGTCACATCAAGGA--- 1380
Qy 419 SerGlyIleProSerGluIlaThrCysIleAsnValIleIlepheAsnAsnIleIleVal 438
Db 1381 -----GAAAGCTTCCTGCAAAATGCAAGTTAAAGGATIAGGCACCGT 1428
Qy 439 Th-ProHISCYs 442
Db 1429 TCTCTTAATGTC 1440

RESULT 9

US-10-437-963-24607 Application US/10437963
; Sequence 24607, Application No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5321)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 24607
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MHT4530_29575C.1
; US-10-437-963-24607

Alignment Scores:
Pred. No.: 5.35e-107 Length: 1182
Score: 1011.00 Matches: 187
Percent Similarity: 69.52% Conservative: 57
Best Local Similarity: 53.28% Mismatches: 105
Query Match: 42.30% Indels: 2
DB: 18 Gaps: 1

RESULT 10

79 GGCAGTAATGTTCAGCTACAGACTGGGCCATGGAGCGGACATGATGAC 138
Qy 92 AsnIleAlphegluglalatpAspGluIleSerArgLysProValInPhe 111
Db 139 ACCAAGCATTGGAGATACTAGCTGAGCTGCTCTCTGCAAACCTGGAGTTG 198
Qy 112 ValValProIleAlaIleIleValGluIleIleThrPheSerIlyProCysArg 131
Db 199 CTATCCCCAAAGCCAGAAATACCTGATCAACACACACTGCTCTGTCATGCAA 258
Qy 132 SerSerIleSerValIlyStilePheGlySerIleGluGluIlaSerSerIleSerAspTyr 151
Db 259 TCAAGCATCTCATGATGTTGAGGTAGTTGTCGCTCTCCAGAGGGTCAGTCG 318
Qy 152 LysAspArg----ArgLeuPheIleIlePheAspSerValGinAsnIleIleValGly 169
Db 319 AGCAGGAGGACCATAGGAACTGACTGATCTGATCAGTGGTGCACGGTCACTGTC 378
Qy 170 GlyIlyGlyIlyIleIleGlyIlyIleIleGlyIlyIleIleGlyIlyIleIleVal 189
Db 379 GTCGTCGCGACCATAGATGATGAACTGCGATGTCGCTCTGTCGCAAACTGAC 438
Qy 190 LysSerIleProCysBarGaspIlaProThrIlaLeuThrPheTrpAsnCysIlyIleAsnIle 209
Db 439 TCAAGCTTCATGCCAGAGCTCACCGACTGACTCTACTCTGCGAAGATCG 498
Qy 210 LysValAsnIleAsnIleIlyAsnIleAsnIleIlyAsnIleIlyAsnIleIlyAsnIle 229
Db 499 AGGTAAGCTATCTGAACTGTCAGTTAAAGGATIAGGCACCGT 1428
Qy 230 ThrAsnValValIaSerAsnLeuMetIleAsnIleAsnIleAspSerProAsnThrAsp 249
Db 619 GATTCATATCACACGGAGCAGAGTCGAGTCGAGCACTGATGTCATGACGACCGG 678
Db 559 ACCGATGTCGATGGTCTCGCTCTGCGATCACAGCACCCAAACACTGAT 618
Qy 250 GlyValHisValSerAsnThrGlnIlyIleGlnIlyIleGlnIlyIleGlnIlyIle 738
Db 679 GATGACTGATGTCATCAGGACGGACCGAACCTCGATGTCAGTCAGTCATGTC 738
Qy 290 GluProGlyHisIlyIleSerIleIleGlyIlyIleSerIleIleGlyIlyIle 738
Db 739 GACCGGGACACGACCATCAGTCGCTGAGTCATTAATCTGAGCTCATGTC 798
Qy 799 AACATGTCGACCTGCAATGTCGCTGAGTCATGTCGCTGAGTCATGTC 858
Db 310 SerAsnValThrValAsnGluIlaLysIleIleIleGlyIlaGluIaGlyIle 858
Qy 330 ThrTrpGlyGlyIlySerglyGlnalaSerAsnIleIlepheLeuAsnValGluMetGln 349
Db 859 ACATGGCAGGGAGGAAGGGTCTCGGAGAACACTCGTCCTCCAGACTGTC 918
Qy 350 AspIlyIlyIleAspGlnAsnIlyIleAspGlnAsnIlyIleAspGlnAsnIlyIle 369
Db 919 ATGTCGACACCCATCATGACAACTACTCGCATCTCCACCCCTGCAAG 978
Qy 370 GlnglnPheSerIlaValIlyIleIleGlyIlyIleGlyIlyIleGlyIlyIle 389
Db 979 CAACGAAATCTGCACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1038
Qy 390 AlaThrIlyValIleIleIleSpheAspCysSerThrAsnSpheProCysGluGlyIle 409
Db 1039 GCATCGAGGAGGACCATCGTCATGTCAGTCAGTCAGTCAGTCAGTCATGGCAAC 1038
Qy 410 MetGluAsnIleAsnIleValGlyGluIle 420
Db 1099 TTGGAAGATGTCATCTACTGTCAGGGAGGA 1131

Sequence 24608, Application US/10437963
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 3B-21(53221B)
CURRENT APPLICATION NUMBER: US/10/437, 963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 24608
LENGTH: 1359
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_29576C.1
US-10-691-374-2 (1-457) x US-10-437-963-24608 (1-1359)

Alignment Scores:
Pred. No.: 9.14e-107 Length: 1359
Score: 1010.00 Matches: 190
Percent Similarity: 70.11% Conservative: 54
Best Local Similarity: 54.60% Mismatches: 102
Query Match: 42.26% Index: 2
DB: 18 Gaps: 1

US-10-691-374-2 (1-457) x US-10-437-963-24608 (1-1359)

Qy 75 ValIleAsnValLeuSerSerpheGlyAlaLysGlyArgPheGlyLysThrTyrAspAsnIleAla 94
Db 154 GTGTCATGATGGCGAACTGGGCTTACGGAGTGGAAATGTGACAGGAGCA 213
Qy 95 PheGluGlnIleTrpAsnGluAlaCysSerSerArgThrProValGlnPheProValPro 114
Db 214 TTGCAAACGCGATGGCTGCAGCTGCCATCTGCACCTCCATGTGTCATCCCA 273
Qy 115 LysAsnLysAsnTyrLeuLeuLysGlnIleThrPheSerGlyProCysArgSerSerIle 134
Db 274 AAGGCAAGGATGACTCTAACACACATACATCTGTCATGCAATCAAGCATC 333
Qy 135 SerVallysIlePheGlySerLeuGluIleSerSerIleSerAspPheLysAspArg 154
Db 334 ACGTCTATGATGAGGGTACGGTGTTCTCCCTCAAAAGAGCTCATGGCAAGGA 393
Qy 155 -----ArgLeuTrpIleAlaPheAspSerValGlnAsnLeuValValGlyGlyGly 172
Db 394 ACTATTAGCGACTGATTATGTCATGGTGAGTGCGCTTACCTGCGGGTGG 453
Qy 173 ThrIleAsnGlyArgGlyGlnValTyrTrpProSerSerCysLysIleAsnIleSerLeu 192
Db 454 ACTGTCATGATGAAACGCCAATTTGGCAATTCTCCAAACGCAATGCAACTT 513
Qy 193 ProCysArgAspAlaProThrAlaLeuThrHeterAsnCysLysAsnLeuIleVal 212
Db 514 CCATGCACTGAGCTCCAAACGCCCTGACATCTTACCTCCATGAAATGAGGAG 573
Qy 213 AsnLeuIleAsnIleSerAsnAlaGlnIleIleIleLysPheSerCysThrAsnVal 232
Db 574 AACCTGAGCTACTAAACAGCAACAACTCCACATGTCAGTGAGGATGCACTGATG 633
Qy 233 ValAlaSerAsnLeuMetIleAsnIleSerAlaLysSerProAspThrAspGlyValHis 252
Db 634 AGGATCTCTACGCTGACAATCACAGCACCAGCACTAGGCCAAACCCACGCGATCCAT 693
Qy 253 ValSerAsnTrpGlnIleIleSerAspThrIleIleGlyThrGlyAspAspCys 272

RESULT 11
US-10-437-963-28561
Sequence 28561, Application US/10437963
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 3B-21(53221B)
CURRENT APPLICATION NUMBER: US/10/437, 963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 28561
LENGTH: 1335
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_33148C.1
US-10-691-374-2 (1-457) x US-10-437-963-28561 (1-1335)

Qy 75 ValIleAsnValLeuSerSerpheGlyAlaLysGlyArgPheGlyLysThrTyrAspAsnIleAla 94

15 GAGAGCAGGAGCTACCTGGCCGAACTCACCTNTCCGCCCTGGAAATCCACATC 214 ; APPLICANT: Kovacic, David K.
 QY ; APPLICANT: Zhou, Yihua
 Db ; APPLICANT: Cao, Yongwei
 135 SerValLysIlePheGlySerLeuGluAlaSerSerLysIleSerAspThrLysAsp--- 153 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 215 AACGTCATGGTGAAGGGGAGCGCTGGTGGCTCCGGAAATGTCGAACTGGAGAGC 274 ; FILE REFERENCE: 3B-21(5322)B
 QY 154 --ArgArgLeuTrpIleAlaLeuThrPheAspSerValGlnAlaSerLeuValGlyGlyGly 172 ; CURRENT APPLICATION NUMBER: US/10/425,115
 Db 275 AACAGGAGGTACRGATGCTCGRCGCGCGTGCAGCTCGCCGCGGCG 334 ; CURRENT FILING DATE: 2003-04-28
 QY 173 ThrIleAspGlyAsnGlyGlyValTrpPheProSerSerCysLysIleAsnLysSerLeu 192 ; NUMBER OF SEQ ID NOS: 369326
 Db 335 ACCATCGACGGCAACGGCAGGGTGGGGAGAACCTCTCGAAATCAACAGGGCCTC 394 ; SEQ ID NO: 33752
 QY 193 ProCysArgAspAlaProThrAlaLeuThrPheTrpAsnCysLysAlaLeuValGlyGly 212 ; LENGTH: 1372
 Db 395 CCTGCAAGGGAGCTCCAAACGGCTGTTCCAAACGTCGCGACACTGGCTGAGCT 394 ;
 QY 173 AsnLeuLysSerIysAsnAlaGlnGlnIleHisIleLysPheGluSerCysThrAsnVal 232 ;
 Db 455 GGCTCTGAAAGATGGTGAACGCCAGCAGATCCACATGTCAGAGGATTCACCGGGTC 514 ;
 QY 233 ValAlaSerAsnLeuMetIleAsnAlaSerAlaLysSerProAsnThrAspGlyValHs 252 ;
 Db 515 GAGCTGGCCACCTGTCATCTGACCCCGCACGCCAACACAGTGAGCTGAGCTGAT 454 ;
 QY 213 ValSerLysSerIysAsnAlaGlnGlnIleHisIleLysPheGluSerCysThrAsnVal 232 ;
 Db 455 GGCTCTGAAAGATGGTGAACGCCAGCAGATCCACATGTCAGAGGATTCACCGGGTC 514 ;
 QY 233 ValAlaSerAsnLeuMetIleAsnAlaSerAlaLysSerProAsnThrAspGlyValHs 252 ;
 Db 515 GAGCTGGCCACCTGTCATCTGACCCCGCACGCCAACACAGTGAGCTGAGCTGAT 454 ;
 QY 253 ValSerLysThrGlnTyroIleGlnIleSerAspThrIleLeuGlyThrglyAspCys 272 ;
 Db 575 ATCACCCACAGCAAGACGTCAACGCTGAGGACTGCGACCTTAAGACAGGGTGA 634 ;
 QY 273 IleSerIleLeuIleSerGlySerGlnAlaSerAlaLeuIleLeuThrPheGlyProGly 292 ;
 Db 635 GTCCTGATCAGGATCGGACCCACGGTTAACGTCACGTCAGCAGCTGGTGGTGGCCCGG 694 ;
 QY 293 HisGlyIleSerIleGlySerIleLeuIleSerGlySerGlyAlaSerGlyIleValAsn 312 ;
 Db 695 CATGGATTACATGGACTTAGGATGACACTGGCTGAGCTGCTGTCGATGAC 754 ;
 QY 313 ThrValAspGlyAlaLysIleIleGlyAlaGluAsnGlyValArgIleGlyThrIleGln 332 ;
 Db 755 TTCACTGACACCGTGACCTCTATGGCACCCACCATGGCTGGATGAGCATGGCAG 814 ;
 QY 333 GlyGlySerGlyGlnAlaSerAsnIleLeuAsnValGluMetGlnAspValIys 352 ;
 Db 815 GGAGGGAGTGTAGACGCCAGGATATCGCTGATCAGACATGGTCACTGAGTCAG 874 ;
 QY 353 TyrProIleIleAspGlnAsnTyrcysAspArgValGluProCys--IleGlnIle 371 ;
 Db 875 AACCAAATATCATGGACCAACTACTGGCTGAGTAAGAATGGCAGACAGG 934 ;
 QY 372 PheSerAlaValGlnIvalysAsnValValTyrgluAlnIleLysGlyThrSerAlaThr 391 ;
 Db 935 GGATCAGCAGGGATGAGCTGGCTTCAGACAGACATGGCAGACAATTTCC 994 ;
 QY 392 LysValAlaIleLysPheAspCysSerThrAsnPheProCysGluGlyIleLeuMetGlu 411 ;
 Db 995 AAGGTGCTCATCTCTGCAACTGCAAGGAACTACCATCTCATTCCTACAG 1054 ;
 QY 412 AsnIleAsnLeu-----ValGlyIleSerGlyLysProSerGluAlaThrCysLysAsn 429 ;
 Db 1055 GATCATCAGCTGGAAATGTCGAAATGACATGT---GCCAGAGGAGTACTTGCCAGAT 1111 ;
 QY 430 ValHisPheAsnAsnAlaGluHisValThrProHis---CysThrSer 444 ;
 Db 1112 GCACAAATGGAGGAATCTGGACAGTGTGTCACACCATGACCCAGC 1159 ;
 RESULT 13 ;
 US-10-425-115-33752 ;
 ; Sequence 33752, Application US/10425115 ;
 ; Publication No. US20040214272A1 ;
 ; GENERAL INFORMATION: ;
 ; APPLICANT: La Rosa, Thomas J.

Db 672 CAGGGAGCCAGGGATAACGCCAAGGACATCACCTTCCAATATGGTTATGCTACGACGTC 731 Qy 352 LysTyrProIleIleLeuAspGlnAsnTyrCysBspArgluProCysIleGlnGln 371 Db 732 ANGAACCGGATAATCATGCCAGAACTACTGGACAAAGGTAAGCCATGGGAGAACAA 791 Qy 372 PheserAlaValAlaValGlnValAsnValValTyrGluAsnIleLysGlyThrSerAlaThr 391 Db 792 GadtCAGCAGTGAGGTAGGGTCGTCCTCAAGAACATTAGAGGAGCAGCAGAAC 851 Qy 392 LysValAlaIleLeuAspPheAspCysSerThrAsnpheProCysGluGlyIleLeuMglu 411 Db 852 ANGAGCCGCATCAGATGACATGAGACGTCGCCATGCAAGGCTACCTTCAG 911 Qy 412 AsnIleAsnLeuValGlyGluSerGlyLys--ProSerGluIleThrCysIleVal 430 Db 912 AGATCCACTGAAATGCCAGGCCAACACAAGGACTGTCAGATGCA 971 Qy 431 HisPheAsnAlaGluHisValThrProHis--CysThrSerLeuGlu 446 Db 972 AATGGACAGAATTGGGACAGITGCCGCCAGCCTGCATCCATRAAG 1022

RESULT 14
US-10-425-114-30261
; Sequence 30261, Application US/10425114
; Publication No. US0040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalec, David K.
; APPLICANT: Screeen, Steven E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; PILE REFERENCE: 38-21(5321)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30261,
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE: OTHER INFORMATION: Clone ID: UC-ZMFLB73002C03_FLI
; OTHER INFORMATION: Clone ID: UC-ZMFLB73002C03_FLI
US-10-425-114-30261

Alignment Scores:
Pred. No.: 1.76e-90
Score: 870.00
Percent Similarity: 70.85%
Best Local Similarity: 50.78%
Query Match: 36.40%
DB: 17
Gaps: 3

US-10-691-374-2 (1-457) x US-10-425-114-30261 (1-1308)

Qy 132 SerSerIleSerValIleLeuGluIleSerLeuGluIleSerAspTyr 151 Db 2 TCCAGCTTCACGTCACGGTGAAGGCACTCTGGTCATGCCAAACCGGCGGGATGG 61 Qy 152 -----LysAspArgArgLeuIleAlaPheAspSerValGlnAsnLeuValValGly 169 Db 62 AGGGCAATGACGGAGGCACTGGATCTGTCGGGACATCCACAACTTACCGTCAC 121 Qy 170 GlyGlyGlyIleAspIleAspGlyIleGlyIleValTrpTrpSerSerCysIleAsn 189 Db 122 Gccgcgtggcccaatcgatggcaacggcagaaatggctgctactcgatcgatcgatcg 181 Qy 190 LysSerLeuProCysGagGagPheProIleLeuLeuLeuLeuLeuLeuLeuLeu 209 Db 182 AAGGCTCTCCCTGCAAGGAGCTCCAGCGCTCTGTCATTCACACTGCTCGACCTG 241

RESULT 15
US-10-437-63-52002
; Sequence 52002, Application US/10437963
; Publication No. US004012334A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalec, David K.
; APPLICANT: Wu, Wei
; APPLICANT: Cao, Yongwei
; APPLICANT: Li, Ping
; APPLICANT: Boukharov, Andrei A.
; APPLICANT: Barbausk, Brad
; APPLICANT: Liu, Wei
; APPLICANT: Boukharov, Andrei A.
; APPLICANT: Barbausk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5321)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 52002
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_54340C.1

GenCore version 5.1.6
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On protein - nucleic search, using frame_plus_p2n model
 Run on: March 4, 2005, 12:56:14 ; Search time 4970 Seconds
 (without alignments)
 4455.540 Million cell updates/sec

Title: US_10-691-374-2
 Perfect score: 2390

Sequence: 1 MYIQNRNSILLITIPASSIS.....VTPHCTTSLEISEDEALLYNY 457

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delect 7.0

Searched: 4708233 seqs, 24227607935 residues

Total number of hits satisfying chosen parameters: 9416466
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:
 -MODEL=frame+P2n.model -DEV=x1D
 -Q=0.5
 -CGN2.1 -USPTO spool_PUS10691374/runat 28022005-120705 20986/app query.fasta_1.647
 -DB=CGN2 -GENERAL -FACTORY -SUPPLY -MINMATCH=0.1 -LOCPC=0 -LOCPEXT=0
 -UNITS=byte -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.ctd -LIST=45
 -DOCALIGN=200 -THR SCOREPCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTTYPE=PRO -NORM=EXT -HEAPSIZE=50 -MINLEN=0 -MAXLEN=000000000
 -USER=US10691374 @CGN 1_1 5600 @runat 28022005 120705 20986 -NCPU=6 -ICPU=3
 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
 -DEV -TIMEOUT=110 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELECT=7

Database :

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2: gb_hg;*
3: gb_in;*
4: gb_on;*
5: gb_ov;*
6: gb_pat;*
7: gb_pn;*
8: gb_pl;*
9: gb_pr;*
10: gb_ro;*
11: gb_bt8;*
12: gb_sy;*
13: gb_mn;*
14: gb_vl;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2390	100.0	1617	8 LERF2	X05655 Tomato mRNA
2	2390	100.0	1621	6 A15981	A15981 L.eucalyptu
3	2390	100.0	1621	6 AXCC62336	AXCC62336 Sequence
4	2390	100.0	1621	8 LERF2AR	X04583 Tomato mRNA

ALIGNMENTS

RESULT 1					
REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	
1	Rogers, H.J.; Allen, R.L.; Hamilton, W.D. and Lonsdale, D.M.	Pollen specific cDNA clones from Zea mays	Biochim. Biophys. Acta 1089 (3), 411-413 (1991)	9116147	
2		Molecular characterization of tomato fruit polygalacturonase	Mol. Gen. Genet. 208, 30-36 (1987)	1859845	
3		Sheehy, R.E., Pearson, J., Brady, C.J. and Hiatt, W.R.	Intercellular communication in tomato fruit development	(bases 1438 to 1438)	
4			Intercellular communication in tomato fruit development		
5			Intercellular communication in tomato fruit development		
6			Intercellular communication in tomato fruit development		
7			Intercellular communication in tomato fruit development		
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42			Intercellular communication in tomato fruit development		
43			Intercellular communication in tomato fruit development		
44			Intercellular communication in tomato fruit development		
45			Intercellular communication in tomato fruit development		

101809 Sequence 1
 A24194 *L.esculentum*
 AR364905 Sequence
 X14074 Tomato gene
 M37304 Tomato poly
 AF15758 Actinidia
 AF04233 Vitis vin
 L06094 Avocado pol
 BT05376 Arabidops
 X66426 P.americana
 AJ250919 Brassica
 AE059467 *Cucumis m*
 AX41263 Sequence
 AX651724 Sequence
 BT05375 Arabidops
 AK11942 Arabidops
 AX651722 Sequence
 X95800 *B.rapa* mRN
 A62402 Sequence 1
 AJ428543 Brassica
 AJ5701 Sequence 5
 AX016328 Sequence
 Z49971 *B.rapa* of
 L7743 *Malus domes*
 AB084461 Pyrus com
 AF138858 *Lycopersici*
 AX146668 *Arabidops*
 AY046002 *Arabidops*
 AK10520 *Oryza sat*
 AP03837 *Oryza sat*
 X77231 *P.persica* p
 AP003837 *Oryza sat*
 AP03748 *Oryza sat*
 AX652801 Sequence

the ARG at bp 51 codes for the only inframe methionine preceding the N-terminal sequence of Pg-2a, it is probable that the mRNA is translated with a 71AA pre-sequence that is subsequently cleaved to give a 41,828D mature protein. Drs. D. Grierson and R. J. H. Smith kindly reviewed (22-PR-1987) by D. Grierson.

FEATURES
Source Location/Qualifiers
1. .1621

/translation="MVIORNSILLIIIFASSISTCRSVIDUNLKFQVYDNLLEOF
AKHDFQAVISYLSKNTESNNIDKDKGKIVNULFEGAKGDCKTYDIAFSQWNEA
CSSRFIVQEVVKPKNLYLKQTFSSCPRSSKISKFLSEANSISDYLKRNLIAP
DSVQNLVUGGGGTNGCQWWMSPSKTKNSKDRAPALPTWNCNKLKNSK
AQOHKIKFESCTNVVASHMINASAKSPNTDGVMVSNTOYIQSDTGTGDDCISV
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BAIJINY" 1758 . 2415

intron /number=1 2416 . 2547

exon /number=2 2548 . 3326

intron /number=2 3327 . 3491

exon /number=3 3492 . 3695

intron /number=3 3696 . 3716

exon /number=4 3717 . 4259

intron /number=4 4260 . 4467

exon /number=5 4468 . 4566

intron /number=5 4567 . 4648

exon /number=6 4649 . 5601

intron /number=6 5602 . 5710

exon /number=7 5711 . 6138

intron /number=7 6139 . 6255

exon /number=8 6256 . 6787

intron /number=8 6788 . 7244

exon /number=9 7244

ORIGIN

Alignment Scores:

Pred.	No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
		1.31e-116	1506.00	24.43%	63.01%	8

US-10-691-374-2 (1-457) x LEPOLYGA (1-7456)

1 NetValleglarginSerleuleleulelelephealaserSerileser 20

Db 1479 ATGGTATCCAGGAGATAGATTCTCTTCATTTCTCTCACTTC 1538

Qy 21 Thrcy**a**rgSerAsnvallelepaspasneupheylsglnvaltryAspAsnleu 40

Db 1539 ACTGTTGAGACGATGTTATGCAATTATTCAAGCTT 1598

Qy 41 GlugingluphealaibAspPheginlayleuserTyrleuserAsnleuglu 60

Db 1599 GACAAGAAATTGCTCATGATTCTCAAGCTATCTTATTGAGCAAATATGAA 1658

Qy 61 SerAsnAsnleaspvalysvalplybsanglyileysvalleasnvalleuser 80

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Qy	269 -----	192	Qy	269 -----
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QY	137 -		QY	199	4237
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QY	141	leuGluIalaSerSerIysIleSerIysAspPheIysAlaGlnLleIhsIleLySpheGluSeCysThrIva	Db	4358	-GlyAspDabCysIleSerIleValSerGlyValH1
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 Db 986 CTTRCCGTTACAGACAACTGGTAAGATACTAACCTACAGGGTCAAGACTGCT 1045
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RESULT 14
 PAPOLYGU PAPOLYGU 1755 bp mRNA linear PLN 11-MAY-1995
 LOCUS PAPOLYGU
 DEFINITION P. americana mRNA for polygalacturonase.
 ACCESSION X66426.1 GI:22630
 VERSION X66426.1
KEYWORDS
 polygalacturonase.
SOURCE
 ORGANISM Persea americana (avocado)
 PERSEAE; Laurales; Lauraceae;
 Spermatophyta; Magnoliidae; Laurales; Lauraceae;
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Persea americana
REFERENCE
 1. (bases 1 to 1755)
 Dopico, B., Lowe, A.L., Wilson, I.D., Merodio, C. and Grierson, D.
 Cloning and characterization of avocado fruit mRNAs and their
 expression during ripening and low-temperature storage
 Plant Mol. Biol. 21 (3), 437-449 (1993)
 MEDLINE
 PUBMED 8095163
REFERENCE
 2. Dopico, B.
AUTHORS
 TITLE Direct Submission
 JOURNAL Submitted (27-MAY-1992) B. Dopico, Univ. of Nottingham, Dept. of
 Physiology & Envir. Sciences, School of Agriculture, Sutton
 Bonington, Loughborough, Leicestershire, LE12 5RD, UK
FEATURES
Source
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CDS

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 Qy 261 IleSerAspThrAlleGlyThrGlyAspAspCysIleSerIleValSerIleSerGln 280
 Db 838 GCTCCATTCCATCTGGACAGGCGATGTTGATCTGATGTTGATGTTGAGGATCAA 897
 Qy 281 AsnValGlnIleThrAsnIleThrCysGlyProGlyHisGlyIleSerIleGlySerLeu 300
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 Qy 301 GlySerGlyAsnSerGlySerIleValSerAlaValThrValAlaGluIleIysIle 320
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 Qy 321 GlyAlaGluIleGlyValArgIleIysThrTrpGlyIleGlySerGlyGlnAlaLaserAsn 340
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 Db 1360 CGTGCAATCC 1371

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